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AX146426 AF153062 S64596 RNCA1T1 BC003198 BC059281 BC050014

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CS080950 Sequence
AX330012 Sequence
AX3330557 Sequence
AX333305 Sequence
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AX411302 Sequence
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GenCore version 5.1.7
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PGPVGVQGPPGPAGEEGKRGARGBFGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPA
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PSPPPCALGOGNG WGFPGPKGANGERGYGERGV PGB PGA PGAGAGNG PROP
AGPAGERGEGAPAGS PGFQCL PGPAGP PGEAG PGGYPGDLGAPGPSGGARGRGF P
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PGDRGEPGPPGPAGPAGPPGADGQPGAKGEPGDAGAKGDAGPPGPPGPPGPPGPPGDV
GAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPPGPPGPAGKEGGKGPRGETG
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GAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPVGPVGARGPAG
PQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGGPSGPSGASGPAGPRGPPGS
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PQEKAHDGGRYYRADDANVVRDRDLEVDTTLKSLSQQI ENIRSPEGSRKNPARTCRDL
KMCHSDWKSGEYWI DPNQGCNLDA I KVPCNMETGETCVY PTQPSVAQKNWY I SKNPKD
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                           1240 TGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCCAAGAGGCTCCA
                                            TGGCCTACATGGACCAGCAGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCA
                                                                                                                               ACGAGATCGAGATCCGCCCCGAGGCCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG
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Patent: WO 0144455-A 1 21-JUN-2001;
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Sequence 1 from Patent WO0144455.
AX167114
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Location/Qualifiers
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Pred. No. 5.3e-138;
0; Mismatches 3;
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                                                                                           5921 bp DNA Sequence 153 from Patent WO2005040414. CS080950 GS080950.1 GI:66348467
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1. .5921
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Best Local Similarity 99.7%;
Matches 944; Conservative
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Pred. No. 5.1e-138;
0; Mismatches 3;
                                                                               Query Match 97.8%;
Best Local Similarity 99.7%;
Matches 944; Conservative
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Patent: WO 0194629-A 521 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers 6728 bp 1 Sequence 521 from Patent WO0194629. 1. .6728 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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Patent: WO 0194629-A 3809 13-DEC-2001;
                                                                                                        ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG 3999
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                    TGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCA
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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    .6728
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Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                        St Croix, B., Kinzler, K.W. and Vogelstein, B. Endothelial cell expression patterns Patent: WO 0210217-A 260 07-FEB-2002; The Johns Hopkins University (US)
                                                                                                                                                                                                                                               Score 942.2; DB 6;
Pred. No. 5.1e-138;
0; Mismatches 3;
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/organism="Homo sapiens"
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Best Local Similarity 99.7%;
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6728 bp I from Patent WO0210217.

AX393330 Sequence 260 f AX393330

RESULT 8
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OPGAKGANGAPGAGPGGPRGSEGPGSSOPGANGASBEGAAGPAGAAGDG
OPGAKGANGAPGAFGARDEPGARGSSOPGAGGBPGPKAKGSBPGANGANGA
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GERGSPGPAGPKGSPGEAGRPGEAGLPGAKGITGSPGSPGPPGANGAPGAPGANGAPGAPGA
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GAPGAKGARGSAGPPGAATGPPGAAGRVGPPGPSGNAGPPGPPGPPGPAGKEGGKGPRGETG
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GAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPVGPVGARGPAG
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DQLSYGYDPRGSTGVPGPRGPSGPPRGLPGPPAPGPGGAGPGPPGBPGASPMG
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Dalgleish,R.
Dalrect Submission
Submitsed (01-JUL-1996) Raymond Dalgleish, Department of Genetics, University of Leicester, University Road, Leicester, University of Leicester, University Road, Leicester, United Kingdom
                                     5 (Dases 4482 to 6728)
Maatta, A., Bornstein, P. and Penttinen, R.P.
Maatta, A., conserved sequences in the 3'-untranslated region of the COLIAL gene bind cell-specific nuclear proteins
FEBS Lett. 279 (1), 9-13 (1991)
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                                                                                                                                                                                                                         The human type I collagen mutation database hucleic Acids Res. 25 (1), 181-187 (1997) 9016532
Biochem. J. 253 (3), 919-922 (1988)

    .6728
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223. .417
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/number=6
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This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan. Totoki Y, Toyoda A, Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan. e-mail: aktanaka@postman.riken.go.jp
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4420 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCCGGACAAC 4479
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None Title
Published Only in Database (2005)
2 (bases 1 to 4721)
Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S.,
Ohara,O., Nagase,T. and F.Kikuno,R.
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Ohara,O., Nagase,T. and F.Kikuno,R.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Homo sapiens mRNA for Collagen alpha 1 chain precursor variant
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/note="Start codon is not identified."
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Pred. No. 5.1e-138;
0; Mismatches 3;
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/citation=[3]
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PGSAGAPGNOGLNGLPGPIGPPGPRSTGDAGPVGPRGPPGPPPGPPGPPSBAGPDFSFL
PQPPQEKAHDGGRYKADDAMVVBDRDLEVDTTLKSLSGQIENIRSPBGSRRNPARTC
RDLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKN
                                                                                                                                                                                                                                                                      PKDKRHVWFGESMTDGFQFEYGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVA
YMDQQTGNLKKALLLQGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTK
TSRLPIIDVAPLDVGAPDQEFGFDVGPVCFL"
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Pred. No. 3.1e-137;
0; Mismatches 6;
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llarity 99.4%;
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Evarchontoglires; Primates; Catarrhini;
ACGAGATCGAGATCCGCGCCGAGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG
                                                                                                                                  CTGGTCCTGTTGGTCCCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGTCCTCCTGGCC
                                                 ACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG
                                                                                                                 GCTGCACGAGTCACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGT
                                                                                                                                                                                 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGAACCAGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corporation (NY) (US)
Location/Qualifiers
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
Hominidae; Homo.
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                                                                                                                                                CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCCAGAGGGAAGCCGCAAGA 312
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Human proalpha 1 (I) chain of type I procollagen mRNA (partial).
K01228
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Collagen; type I collagen.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                             GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCCA
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                                                                                                 GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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                                                AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCCAGTGTGGCCCCAGAAGAACTGGTACA
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Parrar, G.J., Humphries, P., Millington-Ward, S. and Kenna, P.F.
Suppression of polymeric alleles
Patent: WO 03048362-A 16 12-JUN-2003,
College of the Holy and Undivided Trinity of Queen Elizabett
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Hominidae, Homo.

1 (baees 1 to 4752)

2 (Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopking, R.F., Jordan, H., Moore, T., Mar, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Homo sapiens collagen, type I, alpha 1, mRNA (cDNA clone MGC:33668
HMAGE:5264710), complete cds.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                     2549 ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
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CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCCAGAGGGAAGCCGCAAGA
                     2429 CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCNCCCGCAAGA
                                                                             313 ACCCCGCCCCCCCCCCCCCCCCCCCCCCACTCCCACTCGACTGGAAGAGTGGAGAGT
                                                                                                   ACCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGTGGAGT
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MGC.
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Homo sapiens
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The human proalpha 1 (I) chain of type I procollagen is compared with those of calf, rat, mouse and chicken and with the proalpha 2 (I) chain from man. Selective pressure during 250,000,000 years of evolution acted more strongly on the proalpha 1 (I) chain than on the proalpha 2 (I) chain. The alpha 2 (I) chain than on the proalpha 2 (I) chain. The alpha 2 (I) chain domain as sequences are not as highly conserved as those of the C-propeptide domain of the same chain.
                     1 (bases 1 to 3347)
Bernard, M.P., Chu, M.L., Myers, J.C., Ramirez, P., Bikenberry, E.F. and
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                                                        Prockop, D.J.

Nucleotide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procollagen. Statistical evaluation of structures that are conserved during evolution Biochemistry 22 (22), 5213-5223 (1983)
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Submitted (16-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Betheada, MD 20892-2590, USA
NH-MGC Project URL: http://mgc.nci.nlh.gov
On Aug 25, 2003 this sequence version replaced gi:22328091.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Plero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.G.B. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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/product="alpha 1 type I collagen, preproprotein"
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4357 GCTGCACGAGTCACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAGGA 4416
                                                913 TCGGCTTCGACGTTGGCCTGTTCTCTGTAAACTCCCTCCATC 959
        8 6 6 6
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Search completed: April 27, 2006, 20:12:54 Job time : 5492.32 secs

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Aea28568 Human col
Aea28572 Human alk
Aea28576 Human sol
Acc50109 Breast ca
Adg65048 Human col
Adg65048 Human col
Adg65048 Human col
Adg65048 Human col
Adg69586 Human col
Adr29709 Human bre
Aaz2672 Human bre
Aaz6729 Human bre
Aaz6729 Human bre
Ab162184 Colon ade
Ab162194 Human Tum
Ab192119 Human Tum
Ab192119 Human Tum
Ab193151 Gene #394
                                                             April 27, 2006, 17:14:00 ; Search time 602.014 Seconds (without alignments) 10661.049 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                       4996997 seqs, 3332346308 residues
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                                          nucleic search, using sw model
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ADQ19469
ADQ29586
ADR99017
ADZ26572
ADZ09709
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ABL62729
ABL65472
ABL92119
ABN97451
ABV94755
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Maximum DB seq length: 2000000000
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ACT12845 Human Brc
Add14744 Human Brc
Abx72044 DNA encod
                       Abx72044 DNA encod
Adp5588 Human mRN
Adv70139 Tumor-as
Ade87369 Human pan
Ade87389 Human pan
Ade87389 Human cDN
Aas2241 Human cDN
Aas22677 Human cDN
Ads9829 Protein f
Acc46568 Human dit
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Ade87387 Human pan
Acc468618 Human col
Acc46818 Human pan
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Acc46813 Human pan
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Breast ca
                                                                                                                                                                                                                                                                                                                                              protein secretion; fusion protein; protein activation; collagen I; ss;
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/product= "Human collagen alpha(I) C-propeptide TO
construct protein"
/note= "No start codon"
ACC50108
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               ADD14744
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P-PSDB; AEA28569.
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Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
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-propeptide fusion protein"
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                                                     661 GCAAGAACAGCGTGGCCTACATGGACCAGCAGATGGCAACCTCAAGAAGGCCCTGCTCC
                                                                                                                                                                                                   781 TCACTGTCGATGGCTGCACGAGTCACACGGAGCCTGGGGCAAGACAGTGATTGAATACA
                                                                                                                                                                                                                                                                                                                   protein secretion; fusion protein; protein activation; collagen I; ss;
gene; Alkaline phosphatase; gene fusion.
                                                                                                                                                                                                                                                                                                  721 TCAAGGGCTCCAACGAGATCGAGATCCGCGCGAGGGCAACAGCCGCTTCACCTACAGCG
                                                                                                                                                                  TCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACA
                                                                                                                                                                                                                                AAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCC
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                                                          The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion. to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such cationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for maturally occurring trimeric ligands. The current sequence is that of the human collagen alpha(1) C-propeptide TO construct construct includes a partial glycine-repeat triple helical region.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 963 BP; 207 A; 323 C; 256 G; 177 T; 0 U; 0 Other;
                                  Claim 11; SEQ ID NO 1; 47pp; English
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comprising a transcriptional promoter linked to a template encoding a signal peptide acquire followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a tiret polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly concrained benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be cuseful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their metral to recurring trimeric ligands. The current sequence is that of the human placental alkaline phosphatase (AP)-human collagen T0 construct includes a partial glycine-repeat triple helical region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.3%; Score 956.2; DB 14; Length 2487; Best Local Similarity 99.7%; Pred. No. 1.2e-194; Matches 958; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2487 BP; 525 A; 813 C; 728 G; 421 T; 0 U; 0 Other;
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2187 AAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTC 2246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein secretion; fusion protein; protein activation; collagen I; 88;
                                            ACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAA
                                                                                                                                           ACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCCA
                                                                                                                                                                       2367 ACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCA
                                                                                                                                                                                                     903 GACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCCTCCATCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human soluble CD4-collagen alpha(I) C-propeptide T0 fusion cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24. .2123
/*tag=
//raduct= "Human soluble CD4-collagen alpha(I)
propeptide T0 fusion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              AEA28580 standard; cDNA; 2139 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; CD4; gene fusion.
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first polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much righer affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their naturally occurring trimeric ligands. The current sequence is that of the numan soluble CD4-human collagen alpha (I) C-propeptide TO fusion DNA (sCD4-TO) of the invention. The collagen TO construct includes a partial
polypeptide capable of self-trimerization which is heterologous to the
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Sequence 2139 BP; 518 A; 621 C; 590 G; 410 T; 0 U; 0 Other;

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1488 AACCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAG 1547
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                                                                                                                                                                                                                                                                                                                                       1368 GCTACTACCGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC 1427
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                                                                                                                                                                                                                                                                                                    CGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
                                                                           12 AGAICTAACGGICTCCCTGGCCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGAI
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   Length 2139;
                                      0; Indels
Query Match 98.9%; Score 952; DB 14; L
Best Local Similarity 100.0%; Pred. No. 9.1e-194;
Matches 952; Conservative 0; Mismatches 0;
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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide capable of self-trimerization which is heterologous to the first polypeptide to be trimerized, and introducing the construct into a eukaryotic cell. Receptor decoys, e.g. soluble receptors construct into a only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly

Claim 15; SEQ ID NO 9; 47pp; English.

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1908 AACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGAT 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
                                                                                                                                                                                                                                                                          protein secretion; fusion protein; protein activation; collagen I; ss; gene; Tumor necrosis factor; TNF-RII; gene fusion.
                                                                852 TCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human soluble TNF-RII-collagen alpha(I) C-
propeptide T0 fusion protein"
                                                                                                                                                                                                                                                      Human soluble TNF-RII-collagen alpha(I) C-propeptide TO fusion cDNA.
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                                                                                                           912 TICGGCTICGACGTIGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCTAGA
                                                                                                                                                                                                                                                                                                                                                     cocation/Qualifiers
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                                                                                                                                                                                       AEA28576 standard; cDNA; 1734
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/product=
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Synthetic.
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increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their naturally occurring trimeric ligands. The current sequence is that of the human soluble TNF-RII-human collagen alpha (I) C-propeptide TO fusion DNA (STNF-RII-TO) of the invention. The collagen TO construct includes a
                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCGCCCGCACCTGCGTGACCTCAAGATGTGCCACTCTGAAGAGGTGGAGAGT 372
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                                                                                                                               Length 1734;
                                                                                                        Sequence 1734 BP; 358 A; 598 C; 477 G; 301 T; 0 U; 0 Other;
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                                                                                                                                          Pred. No. 1.4e-193;
                                                                                                                               Score 951; DB 14;
                                                                                   partial glycine-repeat triple helical region.
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GACTCAACGGTCTCCCTGGCCCCATTGGCCCCCTGGTCCTCGCGCTCGCACTGGTGATG 3639
1624 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAAT 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
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Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
Pusztai L, Meric F, Sahin A, Mills GB;
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of a marker in a patient sample with that in the control non-breast
cancer sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breast cancer associated cDNA sequence
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2001US-0306501P.
2001US-0325002P.
2002US-0362585P.
2002US-0380391P.
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Mertens M, Monahan JE, N
Bast RC, Hortobagyi GN,
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Best Local Similarity
Matches 944; Conserv
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18-JUL-2001;
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05-MAR-2002;
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ACC50109
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immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

immune; ds; human.

WO2003072827-A1 Ното варієпв.

04-SEP-2003

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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a autoimmune disease or arthritides. The method comprises obtaining the that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal an array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collageninduced arthritis; and reducing the symptoms associated with collageninduced arthritis; The compositions of the invention have the following

Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

Disclosure, Page, 56pp, English.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT

Thorton SL;

Hirsch R,

WPI; 2003-712740/67. GENBANK; NM_000088.

31-OCT-2002; 2002WO-US035433 31-OCT-2001; 2001US-0336220P activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunomodulacory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This polynucleotide represents a DNA sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic

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0; Mismatches 3;
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Matches 944; Conservative
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BP.

ADP65048 standard; DNA; 5921

RESULT 6 ADP65048

(first entry)

12-AUG-2004

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ADP65048;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGGTGGCC 192
                                                                                                                                                                                                 Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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Best Local Similarity 99.7%; Pred. No. 1.4e-191;
Matches 944; Conservative 0; Mismatches 3;
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                                                                  (PROT-) PROTEIN DESIGN LABS INC.
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                     26-NOV-2002; 2002US-0429739P
                                                                                                               Ginsburg WM,
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present DNA sequence represents a human colorectal cancer-associated protein coding sequence of the invention.
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Pred. No. 1.4e-191;
0; Mismatches 3;
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                                                                Sequence 5921 BP; 1068 A; 1879 C; 1763 G;
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Best Local Similarity 99.7%;
Matches 944; Conservative
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                                                                                                                                                                    ACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG
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Maimonis PJ,
I, Molino GA;
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Dwivedi P, Huntress M, Johnson KA, Lewis ME, M
Brown-Shimer SLA, Thiagalingam A, Thibodeau SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; colon cancer; TIMP1; Regl-alpha; colorectal cancer-associated marker; gene; ds
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(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method (M1) for diagnosing breast cancer in a patient. The method comprises comparing the level of cancer in a patient. The method comprises comparing the level of cancer in a postent with that in a normal patient sample, where a difference in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating comprising two or more probes corresponding to genes selected from ADR99121 and the gene products are polypeptides selected from ADR99121 and the gene products are polypeptides selected from ADR99122 and the gene products are polypeptides selected from ADR99121 and the gene products are polypeptides selected from ADR99122. ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are useful for distinguishing between normal and disease tissue. M3 is useful cor monitoring the response of a breast cancer patient to treatment with an anti-cancer agent. M4 is useful for identifying a compound for treating breast cancer. Note: The sequence data for this patent did not form and the printed specification, but was obtained in electronic form when the form with the form when the form when the form with the form with the form when the form with the form when the form with the form with the form with the form when the form when the form with the form
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                                                        ADR99017 standard; DNA; 5921 BP.
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P-PSDB; ADR99144.
REFSEQ; NM_000088.1.
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                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of detecting lineage-specific mRNA in the sample. The methods are useful for determining the clinical outcome of a progenitor cell transfer in a subject, and for identifying or quantifying lineage-specific cells. The present sequence represents a human cDNA that encodes a protein used to identify lineage-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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Pred. No. 1.4e-191;
0; Mismatches 3;
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                                                                                                                                                 (DAND ) DANA FARBER CANCER INST INC.
                                                                                             25-SEP-2003; 2003US-0506221P.
                                                          24-SEP-2004; 2004WO-US031524
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Best Local Similarity 99.7%;
Matches 944; Conservative
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compounds having a curative effect on a neoplastic disease. The curre sequence is that of the human breast cancer marker COL1A1 DNA of the invention which is differentially expressed in neoplastic tissue.
                                                                                                                                                  Gaps
                                                                          Sequence 5921 BP; 1068 A; 1879 C; 1763 G; 1211 T; 0 U; 0 Other;
                                                                                                              Length 5921;
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Pred. No. 1.4e-191;
0; Mismatches 3;
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Best Local Similarity 99.7%;
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The invention relates to detecting differential expression of one or more nucleic acid sequences (appearing as AEA04356-AEA04448 in a biological sample comprising obtaining the sample from a subject, and detecting a change in the expression level of one or more nucleic acid sequences, is nevel to a control expression level of the nucleic acid sequences, is nevel included are detecting cancer (or a pre-malignant condition thereof) in a subject (comprising comparing the expression level of one or more nucleic acid sequences in a biological sample from the subject (and pre-malignant condition) are least two-fold in the expression level of the mucleic acid sequences, where a change of at least two-fold in the expression level of the mucleic acid sequences, where a change of at least two-fold in the expression level of the mucleic acid sequences is indicative of cancer or pre-malignant condition), monitoring the condition) in a subject (by detecting in a biological sample of the aucleic acid sequences, repeating the first step at a subsequent point in time the expression of cancer or a pre-malignant condition in the subject, where a change in the acid sequences, repeating the subject (comprising detecting in a malignant condition in the subject (comprising detecting in a subject the subject the expression level of one or more or more or more or mucleic acid sequences, comparing the expression level of one or more or more or mucleic acid sequences, comparing the expression level of one or more or more or mucleic acid sequences, comparing the expression level of the subject, the expression level of one or more or more or more or more or accept prognosis of the subject based on the comparison), determining the efficacy of a therapy for inhibiting cancer in a subject, a polypeptide encoded by the nucleic acids above the polypeptide sequence, and detecting an authorial as mucleic acids above the polypeptide sequence, and detecting in a biological sample the polypeptide sequence, and detecting a condition or more nucleic 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting expression of one or more nucleic acid sequences in biological sample, useful for detecting cancer, comprises detecting a change in the expression level of one or more nucleic acid sequences relative to a
                                                                                                                                                              Tumor marker; ss; gene; colon tumor; cancer; cytostatic; neoplasm;
diagnostic; microarray; drug screening.
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                                                                                                                       Human cDNA from gene overexpressed in cancer, COLIA1
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Lewis M;
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MAYO FOUND MEDICAL EDUCATION & RES.
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A, Thibodeau
BP.
AEA04387 standard; cDNA; 5921
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                                                                               (first entry)
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Boardman LA,
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P-PSDB; AEA04480.
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NM_000088.
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                                        AEA04387;
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Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGGTGGCC 192
biological sample, which is useful for detecting cancer (especially colon
                cancer), monitoring the onset, progression, or regression of cancer or a pre-malignant condition, or determining prognosis for cancer or its pre-malignant condition in a subject, or for determining the efficacy of a test compound for inhibiting cancer in a subject. The compound is useful for inhibiting cancer in a subject. The antibodies may also be used to treat cancer. The present sequence is a cDNA from a human gene over-
                                                                                                                                                                                                                                                                                                          72
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                                                                                                                                                                                   Sequence 5921 BP; 1068 A; 1879 C; 1763 G; 1211 T; 0 U; 0 Other;
                                                                                                                                                                                                                           Length 5921;
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                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                         Score 942.2; DB 14;
Pred. No. 1.4e-191;
0; Mismatches 3;
                                                                                                                                                                                                                         tch 97.8%; al Similarity 99.7%; 944; Conservative
                                                                                                                                             expressed in cancer samples.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression
and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antisense DNA oligonucleotide useful for inhibiting the of wild type COLIA1 gene, for treating, reducing the risk of, preventing collagen disorders.
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                                                                                        Indels
                                                            Human pro-alpha-1 chain of type I procollagen DNA
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Pred. No. 1.4e-191;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COL1A1 gene; collagen; procollagen; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                      AAF90491 standard; DNA; 6728 BP
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Best Local Similarity 99.7%;
Matches 944; Conservative
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(ASTR ) ASTRAZENECA UK LTD.
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ID NO:521

gene sequence SEQ

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Colon adenocarcinoma related
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 GATCTAACGGTCTCCCTGGCCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGATG
                                          CTGGTCCTGTTGGTCCCCCCCCCCCTCCTGGACCTCCTGGTCCCCCTGGTCCTCCTCCAGCG
                                                                                   CTGGTTTCGACTTCAGCTTCCTGCCCCAGCACCTCAAGAAAGGCTCACGATGGTGGCC
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(first entry)

15-MAY-2002

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SAXEX

DNA;

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ABL62184

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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                               Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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2000US-023413P.
2000US-0234034P.
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2000US-0234503P.
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2000US-0234503P.
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Weaver Z;
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Soppet DR,
                                                                                                                                                                                                           13-DEC-2001
                                                                                               gene; ds.
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to be tested for anti-neoplastic activity, determining a change in cappression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 954 identical to (S), where a change in activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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Gaps Sequence 6728 BP; 1213 A; 2144 C; 1971 G; 1400 T; 0 U; 0 Other; Score 942.2; DB 6; Length 6728; Pred. No. 1.4e-191; 0; Mismatches 3; Indels 0; 97.8%; Query Match Rest Local Similarity 99.7

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2000US-0236842P. 2000US-0236891P. 2000US-0237172P.

2000US-0237295P. 2000US-0237316P. 2000US-0237425P.

02-OCT-2000; 02-OCT-2000; 03-OCT-2000;

4419 4479 912 852 GCTGCACGAGTCACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAGT CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCCAGGAAT CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCCAGACCAGGAAT cancer; colon; breast; ovary; oesophagus; kidney; thyroid; Colon adenocarcinoma related gene sequence SEQ ID NO:1066. reserresacerresecreterererereraaacreereare ABL62729 standard; DNA; 6728 BP (first entry) 15-MAY-2002 793 4420 913 4480 853 ABL62729; RESULT 15 ABL62729 ID ABL6 셤 Š 8 ò 셤

stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; 2000US-0235082P. 2000US-0235134P. 2000US-0235280P. 2000US-0235637P. 2000US-0235638P. 2000US-0235711P. 2000US-0235720P. 2000US-0235840P. 2000US-0235863P. 2000US-0236028P. 2000US-0236032P. 2000US-0236033P. 2000US-0236034P. 2000US-0236109P. 2000US-0236111P. 2000US-0234923P 30-MAY-2001; 2001WO-US010838 2000US-0234034P WO200194629-A2. 18-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 22-SEP-2000; 22-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; Ното варіелв. 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 18-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 28-SEP-2000; 13-DEC-2001 gene; ds.

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03-OCT-2000; 2000US-0237598P.
03-OCT-2000; 2000US-0237604P.
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01-NOV-2000; 2000US-0244867P.
                                                                                                                                                     Augustus M,
Weaver Z;
                                                                                                                       (AVAL-) AVALON PHARM
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Soppet DR,
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3699 3759 ö GCTACTACCGGGCTGATGAGCGAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA 3819 cecrcaadadecreadecadaarecarecadadecenedadecenedadecenada 3879 3880 ACCCCCCCCCCCCCCCCCCCCCCCCAAGATGTCCCACTCTCACTCGAAGAGTCGAGAGT 3939 192 312 432 CTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTGGTCCCTGGTCCTCCAGCG 132 252 CTGGTCCTGTTGGTCCCCCCCCCTCCTGGACCTCCTGGTCCCCTGGTCCTCCTCCTGGCG GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA GATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGATG CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCTCAAGAGAAGGCTCACGATGGTGGCC creditircalcircaectrececeaectreacareagaagactreacgaregreece CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCCAGAGGAAGCCGCAAGA ACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGT ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG Gaps ö 97.8%; Score 942.2; DB 6; Length 6728; 99.7%; Pred. No. 1.4e-191; ive 0; Mismatches 3; Indels 0; Conservative Similarity Local S. 944; 3820 3580 3640 3700 3760 2 73 133 193 253 313 373 Query Match Best Loca Matches g 8 6 음 상 음 8 8 8 셤 ò 8

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Homo sapiens COLIA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 3492)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, W.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
CB194117
CB134286
CB132414
CB12286
CB12484
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CB139456
CB139456
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CB1322293
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Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriars, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, A.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                               Pan troglodytes (chimpanzee)
Ban troglodytes
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Direct Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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1 (bases 1 to 1275)
Shultz, M.A., Zhang, L., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V., Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S.B., Plopper, C.G. and Buckpitt, A.R.
Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shultz MA

Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA .
Tel: 530 752 4698
Emai: 330 752 4698
Emai: mashult-Zeucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred 20) and vector/linker sequence has been removed.
High quality sequence stop: 1275.
Location/Qualifiers
                                                                                 TCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCG
                                                                                                                                                                                                 ACGAGATCGAGGCCCGAGGCCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG
                                                                                                                                         TGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCA
                                                                                                                                                                                                                                                                                                                  CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAAT
                            TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCT
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="Contig3827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
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/note="Organ: lung; Vector: pGEM-112£(-); Site 1: Eco RI; Site 2: Not I; mRNA was isolated from microdissected rat lung—airways and parenchyma tissues."
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                                                                                                                                                                                                                                    83.4%; Score 803; DB 6; L
llarity 90.5%; Pred. No. 2.3e-172;
Conservative 0; Mismatches 90;
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GSS 17-DEC-2003
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mus musculus COLIA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
373 ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
                                                                                                                                                                          493 TCAGCAAGAACCCCAAGGACAAGAGCATGTCTGGTTCGGCGAGAGCATGACCGATGGAŢ
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,N.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Direct Submission Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 302 (5652), 1960-1963 (2003)
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Mus musculus
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                                                                                                                           CF111063 123-JUL-2003 Shultzomica04314 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig3827 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="airway or parenchyma"
/dev stage="adult"
/dev stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="0rgan: lung; Vector: pGRM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shultz WA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred .20) and vector/linker sequence has been removed.
High quality sequence stop: 1275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTACTACCGGGCCGATGATGCCAACGTGGTCCGTGACCGTGACCTTGAGGTGGACACTA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGGCCCAAGAGCCGCAAGA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCAAGAGGCTGAGCCAGCAGATTGAGAACATCCGCAGCCCTGAGGGCAGCCGCAAGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 ACCCCGCCCCCCCTCCCCTCACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGAGT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTCAACGGTCTCCCTGGCCCCATTGGTCCCCCTGGTCCTCGAGGTCGCACTGGCGATA 175
                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Eukaryota, Eutheria, Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 1275)
Ehultz,M.A., Zhang,L., Gu, Y.-Z., Baker,G.L., Fannuchi,M.V.,
Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.
Gene expression analysis in response to lung toxicants: I.
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                          CF111063.1 GI:33167555
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 857; Conserv
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PUBMED
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Contact: Smith TPI
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
Email: smithAeemail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with
          EST 14-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db xref="taxon:9823"
/tishue_type="pooled"
/tlab host="bH10B"
/clone_llb="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibxary made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGGCGGTTTTCGACTTCTAGCTTCTTGCCCCAGCCACCTCAAGAGAAGAGATCACGATGGTGG
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Porcine EST collection using a normalized library constructed embryos representing early developmental stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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1098161 Manc 4PIG Sus scrofa cDNA 5', mnna sequence.
DN103076
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Plate: TWW8073 row: P column: 20
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
1. .867
/organism="Sus gcrofa"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (pig)
Sus scrofa
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Best Local Similarity
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                                      and ordering
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Pred. No. 5.1e-167;
0; Mismatches 97; Indels
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                                        genomic
Rockville, MD 20850, USA
This sequence was made by sequencing gether a lightent.
Location/Qualifiers
1. 3490
/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
<1. .>3490
/gene="COLLA1"
/locus_tag="HCM5321"
                                                                                                                                                                                                                                                                                                                                                  81.0%;
ilarity 89.6%;
Conservative
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838; Conserv
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="MARC 7BOV"
/note="Vector: pcDNA3.1; Site 1: EcoR1; Site 2: Not1;
Library made with RNA pooled from multiple tIssues
including ovary, hindbrain, uterus, and day-30 whole embryos."
                                                                                                                                        GATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGATG
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                                                                                         Score 755.4; DB 8;
Pred. No. 1.5e-161;
0; Mismatches 46;
/lab_host="DH10B"
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llarity 94.5%;
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                       CTTCCTGCGCCTGATGTCCACTGAGGCTTCCCAGAACATCACCTACCACTGCAAGAACAG
                                                                                                                                                                                                                             CGTGGCCTACATGGACCAGCAGAGACTCGCAAGAAGGCCCTGCTCCTCCAGGGCTC
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ATACTGGATTGACCCCAACCAAGGCTGCAACCTGGACGCCATCAAAGTCTTCTGCAACAT
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                                                                      CATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGGAGCATGACCGATGG
                                                                                                                                                                   CTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAG
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DN525976
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
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Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

10. (bases I. 40.769)

11. (Asses I. 40.77.), Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of CDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAG 268
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                                                                                                                                                                                             GCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGG
                                                                                                                                     CTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGG
                                                                                                                                                      CTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGGCAGACTGG
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                  GCATGTTCGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGG
                                                                             CTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGGCCTGATGTCCACCAGGG
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfw@incyte.com.
Location/Qualifiers
1. 769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:960"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                 CD607436 769 bp mRNA lines
56095953H1 FLP Homo sapiens cDNA, mRNA sequence.
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CD607436.1 GI:40255699
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Homo sapiens
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                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Buarchontoglires, Primates, Catarrhini, Moninidae, Homo.

(Dases 1 to 764)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 746.8; DB 7; Length 764;
Pred. No. 1.4e-159;
0; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                       Regenerative Medicine
Geron Corporation
Geron Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 868
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 764 Std Brror: 0.00.
                                                                                                                                                                                                                                            Contact: Brandenberger R
   CN394423
CN394423.1 GI:47382018
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Best Local Similarity 99.6%;
Matches 759; Conservative
                                              Homo sapiens (human)
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/note="oligo dT_primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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ILLUWIGEN MCQ 61545 Katze_MMOV Macaca mulatta cDNA clone
IBIUW:31396 5' similar to Bases 5 to 804 highly similar to human
COLLA1 (Hs.172928), mRNA sequence.
DR768506 BR768506.1 GI:71107312
                                                                                                                                                                                                                                               66 GAGGTGGACACCACCACAAGAGCCTGAGCCAGCAGAATCGAGAACATCCGGAGCCCAGAG
                                                                                                                                                                                                                                                                                              GGAAGCCGCAAGAACCCCGCCCCGCACTGCCGTGACCTCAAGATGTGCCACTCTGACTGG
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                                                                                                                                                                                   CGCGATGGTGGCCGCTACTACCGGGCTGATGATGCC-ATGTGGTTCGTGACCGTGACCTC
                                                                                                                                                                                                                                240 GAGGTGGACACCACCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAG
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                                                                                                    Length 762;
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                                                                                                 ch 76.7%; Score 738.6; DB 7; al Similarity 99.3%; Pred. No. 1e-157; 752; Conservative 0; Mismatches 4;
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1 (bases 1 to 762)

1 standenberger, Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
                         CCGTGACTCAAGATGTCCCACTCTGACTGGAAGAGTGGGAGGTACTGGATTGACCCCAA
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Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 762 Std Error: 0.00.
Location/Qualifiers
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17000425072448 GRN_EB Homo sapiens
CN342438.1 GI:47342372
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/organism="Homo sapiens"
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Regenerative Medicine
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CJ023328
CJ023328 full-length enriched swine cDNA library, adult trachea Sus scrofa cDNA clone TCH01C120012 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamashma,N. and Awata,T.
Okumura,N., Hamashma,N. and Awata,T.
Okumura,Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
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Mithal Genome Laboratory, Genome Research Department
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
                                                                                                                                  CGACGTGGCCATCCAGCTGACTTTCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACAT
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quality bases were trimmed based on the quality values.
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/organism="Sus scrofa"
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                                                                                                                                                                                                                                                                                                                                                                               Email: cmagness@illumigen.com
Sequenced on 2005.04.01. 592 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Enarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
1 (bases 1 to 904)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="Electromax DH10B"
/clone lib="Katze MMOV"
/note="Organ: ovary; Vector: pDONR 222; Site_1: BsrG I;
Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
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                                                                                                                                                                                       Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Biol. 6 (7), R60 (2005)
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                                                                                                                                                                                                                                                                                             Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
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/mol type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:31396"
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BACKWARD: CACTATAGGCCGAATTGGGTA
Insert Length: 904 Std Error: 0.00
Plate: C1000631 row: D column: 06
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  Macaca mulatta (rhesus monkey)
Macaca mulatta
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 796)

1 (bases 1 to 796)

1 (circ. K., Mang. J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                       74.7%; Score 719; DB 6; L. 99.0%; Pred. No. 3.1e-153; ive 0; Mismatches 5;
                                                                                                                                                                                                              CA 94304,
                                                                                                                                                                                                                                                  Location/Qualifiers
1. .796
/organism="Homo sapiens"
                                                                                                                                                                                               Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
Email: gfu@incyte.com.
             GI:40255700
                                       sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      ll Similarity 99.0
755; Conservative
                                                                                                                                                                                     Contact: Fu GK
                                                     Homo sapiens
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CD607437.1
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           /clone="TCHOIC120012"
/tissue_type="trachea"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library,
trachea"
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                                                                                                     Score 722.8; DB 7;
Pred. No. 4.2e-154;
0; Mismatches 42;
  /db xref="taxon:9823"
                                                                                                       / Match 75.1%;
Local Similarity 94.7%;
les 748; Conservative (
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Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Taukuba, Ibaraki 305-8602, Japan
2 Ikenodai, Taukuba, 185-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
Esr project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CJ026934 786 bp mRNA linear EST 22-OCT-2004 CJ026934 full-length enriched swine cDNA library, adult trachea Sus scrofa cDNA clone TCH01E040063 5', mRNA sequence.
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Low quality bases were trimmed based on the quality values.

Location/Qualifiers
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                      226 AGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAAGAAGGCCCTGCTCCTCC 167
                                                                                                                                                                                                                                                                                                                                    664 AGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCA 723
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                               ACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGA 347
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Okumura,N., Hamasima,N. and Awata,T.
Okumura, B. Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
14681463
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844 CCACCAAGTCCTCCCGCCTGCCCATCATCGATGTG 878
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                            GCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACA 118
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                       CCGGAGCCTGGGCAAGACAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCA
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Hominidae, Homo.

1 (bases 1 to 764)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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56087938H1 FLP Homo sapiens CDNA, mRNA sequence.
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/db_xref="texon:9606"
/clone lib="Fire"
/note="Vector: pDrive Cloning Vector"
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3160 Porter Dr., Palo Alto, CA 94304,
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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Shinkai, H.,

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Score 710.8; DB 7;
Pred. No. 2.3e-151;
0; Mismatches 47;
Query Match 73.8%;
Best Local Similarity 94.0%;
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Patent No. 6617431

Sequence 22, Application US/09331347C

Patent No. 6617431

Sequence 22, Application US/09331347C

Patent No. 6617431

APPLICANT: Meristem Therapeutics, S.A.

APPLICANT: Meristem Therapeutics, S.A.

TITLE OF INVENTION: Detaining Such and Their Uses

TITLE OF INVENTION: Obtaining Such and Their Uses

FILE REFERENCE: 1149-3

CURRENT APPLICATION NUMBER: US/09/331,347C

CURRENT PILLIG DATE: 1999-08-17

NUMBER OF SEC ID NOS: 22

SOFTWARE: Patentin version 3.1

SEC ID NO 22

SOFTWARE: Patentin version 3.1

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US-09-614-124B-418
US-09-671-325-418
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; Sequence 215, Application US/09338933
; Patent No. 6488931
; Patent No. 6488931
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REPERBENCE: 210121-4621
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; MUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 215
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Sequence 215, Application US/09404879A

Patent No. 6468546

GENERAL INFORMATION:

APPLICANT: Mitchan, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REPERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOUTHARE: FRAISEQ for Windows Version 3.0

SEQ ID NO 215

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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
APPLICANT: Fring, Gordon S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILLING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
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US-09-216-003A-215
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ORGANISM: Homo sapiens
FEATURE:
FEATURE:
LOCATION: (8)
OTHER INFORMATION: Where n is a, c,
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US-09-216-003A-215
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; Sequence 215. Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: MIACHAM, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Fridakis, Tony N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS; TITLE OF INVENTION: OF OVARIAN CANCER
; TITLE OF INVENTION: OF OVARIAN CANCER
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FBSESEQ for Windows Version 3.0
; SEQ ID NO 215
LENGTH: 590
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| LOCATION: (1)...(590)
| OTHER INFORMATION: n = A,T,C or G
US-09-215-681-215
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US-09-215-681-215
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US-10-198-053-215
Sequence 215, Application US/10198053
Sequence 215, Application US/10198053
Sequence 215, Application US/10198053
Sequence 215, Application US/10198053
SEQUENCE BARRATION: Chaitanya S.
APPLICANT: Barger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE REPERBNG: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT PILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 590
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ORGANISM: Homo sapiens
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Sequence 215, Application US/09667857

Sequence 215, Application US/09667857

Sequence 215, Application US/09667857

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Algate, Paul A.

APPLICANT: Reter, March P.

APPLICANT: Reter, March P.

APPLICANT: Reed, Steven P.

APPLICANT: Reed, Steven G.

APPLICANT: Carter, Darrick

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C5

CURRENT APPLICATION NUMBER: US/09/667,857

CURRENT FILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 4555

COURRENT FILING DATE: 2000-09-20
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US-09-667-857-215
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                                                        GCCCAGAGGGGAAGCCGCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACT
                                                                                          263 GCCCAGAGGGCAGCCGCCAAGAACCCCGCCCCTGCCGTGACCTCAAGATGTGCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-404-879A-192
i Sequence 192, Application US/09404879A
j Patent No. 6468546
i GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOCTUMBER: RestSEQ for Windows Version 3.0
SEQ ID NO 192
LENGTH: S87
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1 LOCATION: (1)...(587)

1 OTHER INFORMATION: n = A.T.C or

US-09-404-879A-122
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Best Local Similarity 98.0°
Matches 539; Conservative
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Sequence 215, Application US/09827271

Patent No. 6962980

GENERAL INFORMATION:

APPLICANT: Farger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; FILE REFERENCE: 210121.4626

CURRENT APPLICATION NUMBER: US/09/827,271

CURRENT PILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 215

LENGTH: 590
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OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(590)
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US-09-827-271-215
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                   472 TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCG
                                                                                                                                                        442 TGGCCCAAAAGAACTGGTACATCAGCAAGAACCCCCAAGGACAAAGAAGATGTCTGGTTCG
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412 TCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 192, Application US/09215681A
| Sequence 192, Application US/09215681A
| Patent No. 652853
| GENERAL INPORMATION:
| APPLICANT: Mitchan, Jennifer L.
| APPLICANT: Frudakis, Tony N.
| APPLICANT: Frudakis, Tony N.
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
| TITLE OF INVENTION: OF OVARIAN CANCER
| FILE REFERENCE: 210121.463
| CURRENT APPLICATION NUMBER: US/09/215,681A
| CURRENT FILING DATE: 1998-12-17
| NUMBER OF SEQ ID NOS: 310
| SOFTWARE: PSESEQ for Windows Version 3.0
| SEQ ID NO 192
| LENGTH: 587
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1 LCCATION: (1)...(587)

2 OTHER INFORMATION: n = A,T,C or G

US-09-215-681-192
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                     GCCCAGAGGGCAGNCGCAAGAACCCCGCCCGCACTGCCGTGACTCAAGATGTGCCACT
                                                                                                                                     TCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCCACTCAGCCCAGTG
                                                                                                                                                             CTCGCGGTCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCCCGGGCCCTCCTGGACCTCCTG
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   GCCCAGAGGGGAAGCCGCAAAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACT
                                                                      TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 192, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.46201
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SEQ ID NO 192
; SEQ ID NO 192
; LENDITH: 587
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Pred. No. 5.7e-113;
0; Mismatches 10; Indels 1
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 98.0%;
Matches 539; Conservative
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ORGANISM: Homo sapien
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TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCCAAGGACAAGAGGCATGTCTGGTTCG
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APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan Algate, Paul A.
APPLICANT: King, Gordon E.
APPLICANT: Fling, Steven P.
APPLICANT: Fanger, Gary Richard
APPLICANT: Redd, Steven B.
APPLICANT: Redd, Steven B.
APPLICANT: Carter, Darrick
APPLICANT: Nedvick, Thomas S.
APPLICANT: Octor, Darrick
ITLE OF INVENTION: DIAGNOSII OF OVARIAN CANCER
ITLE OF INVENTION: DIAGNOSII OF OVARIAN CANCER
ITLE OF INVENTION: UMBER: 120/09/667,857
CURRENT APPLICATION NUMBER: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 192
LENGTH: 87
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Best Local Similarity 98.0%; Pred. No. 5.7e-113;
Matches 539; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                Sequence 192, Application US/09667857; Patent No. 6699664; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or US-09-667-857-192
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                                                                                                                                                                                                                                                                                                                                                 Sequence 192, Application US/09216003A

Patent No. 6670463

GENERAL INFORMATION;
APPLICANT: Mitchen, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
FILE REFERENCE: 210121.45
CURRENT PILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 192
LENGTH: 587
                                                                     TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGAACAAGAGGCATGTTCTGGTTCG 531
                                                                                                                                              GCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCG 591
                   382 TCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTG 441
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Pred. No. 5.7e-113;
0; Mismatches 10;
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COTHER INFORMATION: Where n is US-09-216-003A-192
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Best Local Similarity 98.0%;
Matches 539; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-09-216-003A-192
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                                472 TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCG
                                                                442 TGGCCCAAAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCG
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                                                                                                                                                                                                                                                                                    Sequence 192, Application US/09827271
Patent No. 6962980
GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TITLE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFURARE: FastSEQ for Windows Version 3.0
SEQ ID NO 192
LENGTH: 587
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; OTHER INFORMATION: n = A,T,C or G
US-09-827-271-192
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NAME/KEY: misc_feature
LOCATION: (1)...(587)
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ORGANISM: Homo sapien
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US-09-827-271-192
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                                                                                     CTCGCGGTCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTG
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; Sequence 192. Application US/10198053
; Patent No. 6858710
; GENERAL INPORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
TAPLICANT: FRANGE', Gary R.
APPLICANT: FAIL, Panger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT PILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 624
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COTATION: 276

COTHER INFORMATION: n = A,T,C or
15.10-198-053-192
                                                                                                                                                                                                         ATGTGGCCAT 601
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ORGANISM: Homo sapiens
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US-10-198-053-192
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Qy 532 GCGAGACCATGGATTCCAGTTCGAGTATGGCGGCCCAGGGCTCCGACCCTGCCG 591

Db 502 GCGAGACATGACCGATGGATTCCAGTTCGAGTATGGCGGGCTCCGACCCTGCCG 561

Qy 592 ATGTGGCCAT 601

Db 562 ATGTGGCCAT 501

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5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

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(c) 1993 - 2006 Biocceleration Ltd.
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Sequence 1, Application US/10677877A; Sequence 1, Application US/10677877A; Sequence 1, Application NO. US20050202537A1; Sequence 1, Publication No. US20050202537A1; Septimental INFORMATION:

APPLICANT: Liang, Peng, GenHunter Corporation

TITLE OF INVENTION: Methods and composition for producing secreted trimeric;

TITLE OF INVENTION: Methods and biologically active fusion proteins; FILE REFERENCE: 03-052-PL

CURRENT PAPLICATION NUMBER: US/10/677,877A;

CURRENT PILING DATE: 2003-10-02; NUMBER OF SEQ ID NO 1

LENGTH: 963

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

FEATURE:
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Sequence 5, Application US/10677877A
Sequence 5, Application US/10677877A
Sequence 5, Application US/2005020537A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL
CURRENT APPLICATION UNDERE: US/10/677,877A
CURRENT RILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 5
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ORGANISM: Homo sapiens
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US-10-677-877A-5
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Federace 9, Application US/10677877A
Fublication No. US20050202537A1
Fublication No. US20050202537A1
FUBLICANT: Liang, Peng; GenHunter Corporation
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: Teceptor analogs and biologically active fusion proteins
TITLE REPERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 16
; EINGTH: 1734
 2028 TCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAA 2087
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (18)...(1718)
US-10-677-877A-9
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                             RESULT 4
US-10-677-877A-9
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          APPLICANT: Liang, Peng, GenHunter Corporation
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                   1188 AGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGAT 1247
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.'
Matches 952; Conservative
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                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
SENERAL INFORMATION:
                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (24)
US-10-677-877A-13
                                                                                                                                LENGTH: 2139
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                                                                                                         Score 942.2; DB 6;
Pred. No. 7.3e-255;
0; Mismatches 3;
                                                                                                           Query Match
Best Local Similarity 99.7%;
Matches 944; Conservative
                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-177-293-66
LENGTH: 5921
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APPLICANT: Gannavarpu, Manjula
APPLICANT: Gannavarpu, Maureen
APPLICANT: Manetens, Maureen
APPLICANT: Mertens, Maureen
APPLICANT: Mag, Youknen
APPLICANT: Mag, Youknen
APPLICANT: Myer, Vic
APPLICANT: Myer, Vic
APPLICANT: Myer, Vic
APPLICANT: Mag, Youknen
APPLICANT: Mayers, Rachel E
APPLICANT: Mayers, Rachel E
APPLICANT: Mayers, Rachel I
APPLICANT: Mayers, Rachel I
APPLICANT: Mayers, Rachel I
APPLICANT: Mario, Youngay
APPLICANT: Mario, Tonda
APPLICANT: Mario, Tonda
APPLICANT: Manils, Gordon B
APPLICANT: Mils, Gordon B
APPLICANT: Mild DATE: 2001-06-21
APPLIOR FILING DATE: 2001-06-21
APPLIOR FILING DATE: 2001-07-39
APLIOR FILING DATE: 2001-07-39
APLIOR FILING DATE: 2002-03-05
APPLICANTION UNMER: US 60/325,002
APPLICANTE APPLICANTION UNMER: US 60/325,002
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                                               1324 TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCT 1383
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                     TCCAGTTCGAGTATGGCGGCCAGGCTCCGACCTGCCGATGTGGCCCATCTGCAGCTGACCT
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Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
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US-10-764-425-18

US-10-764-425-18

Sequence 18, Application US/10764425

Publication No. US20040146921A1

GENERAL INFORMATION:

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Bigwood, Douglas

APPLICANT: Taylor, Iam

APPLICANT: Taylor, Iam

TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE

FILE REFERENCE: 515.

CURRENT PAPLICATION NUMBER: US/10/764,425

CURRENT PAPLICATION NUMBER: 60/442,582

PRIOR PRING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 191

SEQ ID NO 18

SEQ ID NO 18

LENTH: 5921
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TCAGCAAGAACCCCAAGGACAAGAGCCATGTCTGGTTCGGCGAGAGCATGACCGATGGAT
                                                                                                          TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCT
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US-10-764-425-18
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                                            US-10-301-822-29

Sequence 29, Application US/10301822

Publication No. US20030148410A1

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Gaillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Mundan, John E.
APPLICANT: Margart, Lawrence J.
APPLICANT: Mranthon: Novel Genes, ComPositions, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERRAPY OF COLON CANCER
TITLE OF INVENTION: THERRAPY OF COLON CANCER
TITLE OF INVENTION: THERRAPY OF COLON CANCER
TITLE OF INVENTION: THERRAPY OF COLON CANCER
TITLE OF INVENTION WHERE: US/10/301,822
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR PELING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PELING DATE: 2002-03-05
PRIOR SPECIAL OF SEQ ID NOS: 228
SOFTWARE: PRESENCE PRESEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (120)...(4514)
US-10-301-822-29
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253
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; Sequence 2288, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INDORARIYON:
    APPLICANT: Alacation Methods of TILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators; TILE REFERENCE: 05882.0133.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PILING DATE: 2003-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 22881
     1360 GCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGT 4419
                                                        CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGCCCCCAGCAAT 4479
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99.7%; Pred. No. 7.3e-255;
iive 0; Mismatches 3;
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Matches 944; Conservative
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; ORGANISM: Homo sapiens
US-10-723-860-2288
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                       BREAST CANCER AND METHODS
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APPLICANT: Bigwood, Douglas
TITLB OF INVENTION: EXPRESSION PROFILES FOR BRI
FILE REFERENCE: 5152
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/450,655
PRIOR APPLICATION NUMBER: 20 60/450,655
NUMBER OF SEQ ID NOS: 254
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                  Query Match 97.8%;
Best Local Similarity 99.7%;
Matches 944; Conservative
                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-788-792-23
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; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMANOID ARTHRITIS
; FILE REFERENCE: 10872.514646
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR PILIATION NUMBER: US 60/336,220
; PRIOR PILIATION NUMBER: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FREUSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 5921
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Pred. No. 7.3e-255;
0; Mismatches 3;
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al Similarity 99.7%;
944; Conservative
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US-10-287-436A-139
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US-10-287-436A-139
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Matches 944
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; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: WOUTHS, William
; TITLE OF INVENTION: NUCLBIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: NUCLBIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: UNDER: US/10/956,157
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 340
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                                                                                        TCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAACAACAGCG
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Pred. No. 7.3e-255;
0; Mismatches 3;
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Best Local Similarity 99.7
Matches 944; Conservative
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; ORGANISM: Homo sapiens
US-10-956-157-340
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US-10-956-157-340
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PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
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; ORGANISM: Homo sapiens
US-09-954-456-782
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Best Local Similarity
CURRENT FILING DATE:
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Batent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
FITLE OF INVENTION: Sets
FILE REPRENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
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GACTCAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGATG 3639
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US-09-954-456-782
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3879 3699 3819 3939 4059 192 252 312 1940 ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG 3999 TCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGAT 4119 132 432 492 72 GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA CTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTGGTCCCCTGGTCCTCCTAGGCG 1820 CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGGAAGCGCGCAAGA 1000 Agactogragacctgcgrgraccccactcagcccagrgrgccccagaagaactggraca 13 GATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCTGGTGATG CTGGTCCTGTTGGTCCCCCCCCGGCCCTCCTGGACCTCCTGGTCCCTGGTCCTCCCAGCG CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGGTGGCCC GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACCACA CCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGAAGCCGCAAGA ACCCCCCCCCCCCTCCTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGT Accedecedecergecercangargreecacrergacregaagagreeagagagreer TCTGCAACATGG AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACA TCAGCAAGAACCCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGGATGACCGATGGAT TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCT Gaps ö Length 6728; Indels 373 ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGT Score 942.2; DB 3; Pred. No. 7.5e-255; 0; Mismatches 3; 4060 4120 셤 \$

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3820 cccrcaagagccrgagccagcagarcgagaacarccggagcccagagggaagccgcaaga 3879
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                                                                                                                                            373 ACTGGATTGACCCCAACCAAGGTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
                                                                                                                                                                          313 ACCCCGCCCCCCCCCCCCGCGTGACCTCCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGGGT
                                                                            433 AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACA
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; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Bard St. Croix
; APPLICANT: Bard St. Croix
; APPLICANT: Bard St. Croix
; APPLICANT: Bard Wogelstein
APPLICANT: Reneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT PILING DATE: 2001-08-01
; PRIOR PAPLICATION NUMBER: 60/222,599
; PRIOR PAPLICATION NUMBER: 60/224,360
; PRIOR PILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; RIOR APPLICATION NUMBER: 60/224,360
; RIOR FILING DATE: 2000-08-11
; NUMBER: OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 6728
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ORGANISM: Homo sapiens
US-09-918-715-260
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       TCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCG
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                                                                                                                 TGGCCTACATGGACCAGCAGCTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCA
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JAPPLICANT: Horne, Darci T.
JAPPLICANT: Vockley, Joseph G.
JAPPLICANT: Scharf, Uwe
JAPPLICANT: Scharf, Uwe
JAPPLICANT: Gene Logic, Inc.
JTILE OF INVENTION: Gene Expression Profiles in Liver Cancer:
TILE REFRENCE: 4421-5028-WO
JCURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
JPRIOR FILING DATE: 2000-06-14
JPRIOR FILING DATE: 2000-06-14
JPRIOR FILING DATE: 2000-10-02
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US-09-880-107-3946
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Pred. No. 7.5e-255;
0; Mismatches 3;
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; Sequence 3946, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 944; Conservative
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ORGANISM: Homo sapiens
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                                  CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAGGCTCACGATGGTGGCC
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                   Gaps
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 Length 6728;
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Score 942.2; DB 3;
Pred. No. 7.5e-255;
0; Mismatches 3;
Query Match
Best Local Similarity 99.7%;
Matches 944; Conservative
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Sequence 1003, Ap Sequence 1018, Ap Sequence 1018, Ap Sequence 1022, Ap Sequence 1022, Ap Sequence 1014, Ap Sequence 1014, Ap Sequence 994, App Sequence 972, App Sequence 972, App Sequence 972, App Sequence 972, App Sequence 462, App Sequence 6, Appli

US-11-108-172-966 US-11-108-172-1003 US-11-108-172-1018 US-11-108-172-1015 US-11-108-172-1005 US-11-108-172-1019 US-11-108-172-1019 US-11-108-172-1019 US-11-108-172-994 US-11-108-172-996 US-11-108-172-996 US-11-108-172-972 US-11-108-172-972 US-11-108-172-1007 US-11-108-172-1007 US-11-202-057-4 US-11-202-057-4 US-11-202-057-4 US-11-202-057-4 US-11-202-057-4 US-11-202-057-4 US-11-108-172-985 US-11-091-883-109 US-11-091-883-109

66932 66931.6 6618.2 66

Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 245, App Sequence 1001, Ap Sequence 1001, App Sequence 100, App Sequence 109, App Sequence 109, App Sequence 1996, App

US-10-821-234-579

342.8 340.6

ALIGNMENTS

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Sequence 29, Application US/11186284; Publication No. US20050266493A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                   April 27, 2006, 18:58:56; Search time 662.548 Seconds (without alignments) 5902.968 Million cell updates/sec
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1: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

2: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

3: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

4: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

5: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

7: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

8: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

9: SIDS5/ptodata/1/pubpna/USOB NEW PUB.seq:*

10: SIDS5/ptodata/1/pubpna/USIO NEW PUB.seq:*

11: SIDS5/ptodata/1/pubpna/USIO NEW PUB.seq:*

12: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

13: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

14: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

15: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

16: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

17: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

18: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*

18: SIDS5/ptodata/1/pubpna/USII NEW PUB.seq:*
                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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APPLICANT: Millenniuw Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Money, Genes, Councer, Stephen N.
APPLICANT: Money, Genes, Councer, John E.
TITLE OF INVENTION: METARY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
FILE REFERENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/381,978
PRIOR FILING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-05-05
PRIOR PLING DATE: 2002-05-05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: S21
LENGTH: S21 97.8%; Score 942.2; DB 14; Length 5921; 99.7%; Pred. No. 2.8e-225; ive 0; Mismatches 3; Indels 0; Query Match Best Local Similarity 99.7 Matches 944; Conservative ; NAME/KEY: CDS ; LOCATION: (120)...(4514) US-11-186-284-29 ORGANISM: Homo Sapiens TYPE: DNA Sequence 244, Applesequence 7, Appli Sequence 479, Appli Sequence 106, Apple Sequence 106, Apple Sequence 1017, Apple Sequence 1195, Apple Sequence 81, Apple Sequence 826, Apple Sequence 826, Apple Sequence 826, Apple Sequence 826, Apple Sequence 3354, Apple Sequence 3354, Apple Sequence 3354, Apple Sequence 991, Apple Seque Sequence 138, App Sequence 27, Appl Sequence 1, Appli Sequence 29, Appl US-11-000-463-7 US-11-000-463-7 US-11-001-883-105 US-11-091-883-105 US-10-784-004-1017 US-10-784-004-1195 US-10-784-004-1195 US-10-784-004-215 US-10-784-004-215 US-10-784-004-215 US-10-784-004-215 US-10-784-004-215 US-11-113-557-3354 US-11-108-172-991

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Sequence 138, Application US/10501035
Publication No. US20060046249A1
GENERAL INFORMATION:
THE Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING

RESULT 2 US-10-501-035-138

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TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES FILE REPERENCE: D0185 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR PAPLICATION NUMBER: US 60/350,061
PRIOR PAPLICATION NUMBER: US 60/350,061
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SSQ ID NO 138
LENGTH: 6728
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                                                                                                                                                                                                      Length 6728;
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Pred. No. 2.8e-225;
0; Mismatches 3;
                                                                                                                                                                                                      97.8%;
                                                                                                                                                                                                                 Best Local Similarity 99.7
Matches 944; Conservative
                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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                                           733 ACGAGATCGACCCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG 792
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                                                                                                                                                                                                                                                                   493 TCAGCAAGAACCCCAAGGACAAGAGCATGTCTGGTTCGGCGAGAGCATGACCGATGGAT
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Sequence 1, Application US/11021603
Publication No. US2066003954A1
GENERAL INFORMATION:
APPLICANT: Beri, Rajinder
FILLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
FILE PETERENCE: 06275-254US1
CURRENT FILING DATE: 2004-12-21
PRIOR PELING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/11/49,352
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1000-12-12
PRIOR FILING DATE: 1090-12-13
PRIOR FILING DATE: 1090-12-15
PRIOR FILING DATE: 1090-12-15
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SOFTWARE: PATENTING DATE: 1090-12-15
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NAME/KEY: CDS
LOCATION: (120)..(4511)
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NAME/KEY: sig_peptide
LOCATION: (120)..(185)
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APPLICANT: MILEMINIM FIRETRACEUTICALS, INC.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Thiodeau, Stephen N.
APPLICANT: Thiodeau, Stephen N.
APPLICANT: Thiodeau, Stephen N.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRICER TILING DATE: 2005-07-21
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 228
                                                                       4420 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGCCCCCAGGACTAT9
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4360 GCTGCACGAGTCACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGT 4419
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llarity 99.7%; Pred. No. 2.8e-225;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                   sequence 27, Application US/11186284; Publication No. US20050266493A1
EMBRAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (120)...(4514)
US-11-186-284-27
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Matches 944;
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Sequence 244, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US/00-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 244
LENGTH: 4749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.3%; Score 937.4; DB 8; Best Local Similarity 99.4%; Pred. No. 4.3e-224; Matches 941; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                          CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGGTGGCC 3759
                                                                                                                                                                                                                                                                                                                                                                                                                             AGACTIGGTGAGACCTGCGTGTACCCCCACTCAGCCCAGTGTGGCCCCAGAAGAACTGGTACA 4059
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                                                     Length 6728;
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                                                          14;
                                                   Score 942.2; DB 14;
Pred. No. 2.8e-225;
0; Mismatches 3;
                                                   97.8%;
                                                   Query Match
Best Local Similarity 99.7
Matches 944; Conservative
             JS-11-021-603-1
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                                         CTGGTTTCGACTTCACGCTTCCTGCCCCAGCCACCTCAAGAAAAGGCTCACGGTGGTGGCC
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; Sequence 479, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wehrman, Tom
APPLICANT: Abnang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
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                                                                                                       4360 GCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAACAAAA 4419
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ACGAGATCGAGACCGCGCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATG
                                                                               GCTGCACGAGTCACCGGAGCCTGGGCCAAGACAGTGATTGAATACAAAACCACCAAGT
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APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Chen, Vinod
APPLICANT: Qian, Xiaohong B.
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wehrman, Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Ade
APPLICANT: Drmanac, Ade
APPLICANT: Drmanac, Ade
APPLICANT: Drmanac, Sadoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLUE KEFKEKENET, 782CLP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR PILING DATE: 2004-11-29
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/921,404
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-07-17
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
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; LOCATION: (140)..(4531)
US-11-000-463-7
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (758)..(758)
OTHER INFORMATION: a, c, g
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LOCATION: (768)..(775)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (777)..(782)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (760)..(760)
OTHER INFORMATION: a, c,
FEATURE:
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OTHER INFORMATION: a, c,
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NAME/KEY: modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4040 AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACA 4099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8620 GACTCAACGGTCTCCCTGGCCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCGCTCGTGATG 3679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAAGGCTCACGATGGTGGCC 3799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCGCCCGCACTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGGT 3979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 ACCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGT 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTCAAGAGCCTGAGCCAGCAGCAGCAGAACATCCGGAGGCCCAGAGGGAAGCCGCAAGA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCCAGTGTGGCCCCAGAAGAACTGGTACA 492
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-35
PRIOR PLING DATE: 2000-01-35
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-09-15
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Pred. No. 4.3e-224;
0; Mismatches 6; Indels
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| LOCATION: (1)...(4791)

| OTHER INFORMATION: n = a,t,c or g

US-11-000-463-479
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Best Local
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APPLICANT: FERNANCE SENILLO O.
APPLICANT: FERNANCE SENILLO O.
APPLICANT: SCORAS, ARIF
APPLICANT: CROSEY, JAVIER H.
APPLICANT: CROSEY, JAVIER H.
APPLICANT: CROSEY, JAVIER H.
TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN TITLE OF INVENTION: VABILITY
FILE REFERENCE: 53942US
CURRENT FILING DATE: 2005-03-29
RIOR APPLICATION NUMBER: US/11/091,883
PRIOR APPLICATION NUMBER: 06/556,875
PRIOR APPLICATION NUMBER: 2005-03-29
NUMBER OF SEQ ID NOS: 513
SSOFTWARE: Patentin version 3.3
SEQ ID NO 105
LENGTH: 6741
                                                                                                                                                                                     1160 TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGGCCATCCAGCTGACCT 4219
                                                                           4460 CCTCCCGCCTGCCCATCATGTGGCCCCCTTGGACGTTGGTGCCCCCAGGAAT 4519
                                                                                                                                                                                                                                                            792
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                                                   613 TCCTGCGCCTGATGTCCACCGGGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGG
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Publication No. US20060024693A1
GENERAL INFORMATION:
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                                             NAME/KEY: modified base
LOCATION: (812)..(812)
OTHER INFORMATION: a, c, g, o
FRATURE:
NAME/KEY: modified base
LOCATION: (928)..(928)
OTHER INFORMATION: a, c, g, o
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: modified base
LOCATION: (1501)...(1501)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1841)...(1841)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1892)...71892)
OTHER INFORMATION: a, c, g,
                                                                                                                                                                  FEATURE:
NAME/KEY: modified base
LOCATION: (1203)..(1203)
OTHER INFORWATION: a, c, g,
                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: modified_base
LOCATION: (1207).
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1420)..(1424)
OTHER INFORMATION: a, c, g,
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified base
LOCATION: (1485)..(1485)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1931)..(1938)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1940)..(1948)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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LOCATION: (2871)..(72871)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (3020)..(3020)
OTHER:INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c,
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LOCATION: (1692)...(1692)
OTHER INFORMATION: a, c,
LOCATION: (810)..(810)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
LOCATION: (3380)..(3380)
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3102 CTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGTCCTCCCAGCG 3043 3162 GACTCAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGATG 3103 CTGGTTTCGACTTCCAGCTTCCTNCCCCAGCCACCTCCAAGAGAAGGCTCACGATGGTGGCC 2983 2862 ACCCGCCCGCCCGCCGTGCCTCAAGATGTGCCCACTCTGAACAAGAGTGGAAGT 2803 2802 ACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG 2743 2622 TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCTGCCGATGTGGCCATCCAGCTGACCT 2563 2562 TCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCG 2503 2263 192 GCTACTACCGGGCTGATGATGATGCCAATGTGCTTCGTGACCGTGACCCTCGAGGTGGACCACCA 2923 372 432 612 672 732 193 GCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA 252 733 ACGAGATCGAGATCCGGCCCAGGGGCAACAGCGCTTCACCTACAGCGTCACTGTCGATG 792 253 CCCTCAAGAGCCTGAGCCAGAGATCGAGAACATCCGGAGCCCCAGAGGGAAGCCGCAAGA 312 793 GCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGT 852 853 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCCAGACCAGGAAT 912 373 ACTIGATICACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG 673 TGGCCTACATGGACCAGCAGCAGCATGGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCA 13 GATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTGATG CTGGTTTCGACTTCAGCTTCCTGCCCCCAGCCTCAAGAGAAGGCTCACGATGGTGGCC 493 TCAGCAAGAACCCCAAGGACAAGAGCATGTCTGGTTCGGCGAGAGCATGACCGATGGAT 553 TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCTGCCGATGTGGGCCATCCAGCTGACCT 613 TCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCG Gaps ö Query Match 97.2%; Score 936; DB 14; Length 6741; Best Local Similarity 99.2%; Pred. No. 1e-223; Matches 939; Conservative 0; Mismatches 8; Indels 0 ; OTHER INFORMATION: a, c, g, or t US-11-091-883-105 133 2982 73 3042 셤 셤 g 셤 g 셤 셤 g ઠ ઠે ò Š 셤 ઠ 셤 ð 셤 Š 8 셤 ò 셤 ò 셤 Š ò ò ઠે 용 Š ò

RESULT

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3162 GACTCAACGGTCTCCCTGGCCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCGGTCGTGATG 3103
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OTHER INFORMATION: a, c, g, or t
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LOCATION: (3020)..(3020)
OTHER INFORMATION: a, c,
LOCATION: (1501)..(1501)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
LOCATION: (1542)...[1545)
OTHER INFORMATION: a, c,
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LOCATION: (1692)..(1692)
OTHER INFORMATION: a, c,
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LOCATION: (1841)..(1841)
OTHER INFORMATION: a, c,
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OTHER INFORMATION: a, c,
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NAME/KEY: modified base
LOCATION: (1931)..(1938)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
LOCATION: (1940)..(1948)
OTHER INFORMATION: a, c,
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LOCATION: (2009)..(2009)
OTHER INFORMATION: a, c,
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LOCATION: (2871)..(2871)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
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OTHER INFORMATION: a, c,
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         Sequence 106, Application US/11091883

Publication No. US20060024693A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CIBELLI, JOSE
APPLICANT: FERNANDEZ, EMILIO O.
APPLICANT: KOCABAS, ARIE
APPLICANT: CROSBY, JAVIER A.
TITLE OF INVENTION: LORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN TITLE OF INVENTION: VABILITY
FILE REFERENCE: 53942US
CURRENT APPLICATION NUMBER: US/11/091,883
CURRENT APPLICATION NUMBER: 60/556,875
PRIOR PILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 513
SEQ ID NO 106
LENGTH: 6741
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NAME/KEY: modified base
LOCATION: (758)...(758)
OTHER INFORMATION: a, c, g, or t
FEATURE:
FEATURE:
MAME/KEY: modified base
LOCATION: (760)...(760)
OTHER INFORMATION: a, c, g, or t
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CCATION: (1485).. [1485)
OTHER INFORMATION: a, c, g, or t
FEATURE:
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NAME/KEX: modified base
LOCATION: (928). (928)
OTHER INFORMATION: a, c, g, or t
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LOCATION: (777)..(782)
OTHER INFORMATION: a, c, g, or
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NAME/KEY: modified base
LOCATION: (762)..(766)
OTHER INFORWATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1420)...(1424)
OTHER INFORMATION: a, c, g,
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LOCATION: (1203)..(1203)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1207)...(1207)
OTHER INFORMATION: a, c, g,
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LOCATION: (810)..(810)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c,
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ORGANISM: Homo sapiens
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                                                 Indels
                            Score 934.2; DB 7;
Pred. No. 2.7e-223;
0; Mismatches 8;
                             97.0%;
                            Query Match
Best Local Similarity 99.2
Matches 939; Conservative
; ORGANISM: human
US-10-784-004-1017
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0; Mismatches 8;
Figurence 1195, Application US/10784004
Publication No. US20060084066A1
GENERAL INFORMATION:
TITLE OF INVENTION: Surrogate Markers of Pair FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT PILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 4752
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Best Local Similarity 99.2%;
Matches 939; Conservative
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Db 3968 TCCAGTTCGAGTATGGAAGGTTCCGATCCTGCCGATGCTGCAGCTGCACCT 4027	Db 4268 CCTCCGGCTGCCCATCATCATCATCATCATCATCATCATCATCATCATCA	GENERAL INFORMATION: APPLICANT: Biogen Idec TITLE OF INVENTION: Surrogate Markers of Pain FILE REFERENCE: 08201.6029-00000 CURRENT APPLICATION NUMBER: US/10/784,004 CURRENT FILING DATE: 2004-02-20 NUMBER OF SEQ ID NOS: 1251	Facentin Version 5.2 15 721 rat -215 83.2%: Score		Qy 73 CTGGTCCTGTTGGTCCCCCGGGCCTCCTGGACCTCCTGGTCCCCTGGTCCTCCAGCG 132	Db 3548 GTGGTTATGACTTCCTGCCTCAGCCACCTCAAGAAGACTCTCAAGATGGTGGCC 3607 Qy 193 GCTACTACGGGGTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCA 252	Db 3608 GTTACTACCGGGCCGATGATGACCTGGGCCTGACCCTGACCTTGAGGGGAAGCCGAAGA 3667 Qy 253 CCCTCAAGGCCTGAGCCAGCAGAAACATCGGGAACCCAGAGGAAAGCCGCAAGA 312	Db 3668 CCCTCAAGAGCCTGAGCCAGCAGATTGAGAAACATCGGCAGCCCTGAGGCAGCCGCAAGA 3727 Qy 313 ACCCGGCCGGCACCTGACGTGACTGTGACTCTGACTGGAAGAGTGGAAGAGT 372	Db 3728 ACCCGCCGCACATGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGCGGAGAGT 3787
Qy 793 GCTGCACGAGTCACACCGGAGCCTGGGCCAAGACTGATTGAATACAAACCACCAAGT 852 Db 4357 GCTGCACGAGTCACACCGGAGCCTGGGCCAGGATTGATTG	1.6029-00000 NUMBER: US/10/784,004 2004-02-20 : 1251 ersion 3.2	Query Match 83.2%; Score 801.4; DB 7; Length 5721; Best Local Similarity 90.4%; Pred. No. 3.8e-190; Matches 856; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Qy 13 GATCTAACGGTCTCCTGGCCCCTTGGGCCCCTGGTCGTCGTGGTGATG 72 Db 3428 GACTCAACGGTCTCCTGGCCCCATTGGTCCTCGAGGTCGTCGTGGCGATA 3487	Qy 73 CTGGTCCTCTTGGTCCCCCGGCCTCCTGGACCTCCTGGTCCTCCAGCG 132 Db 3488 GTGGTCTGCTGGTCCCCCGGGACCTCCTGGACCTCCCGGTCCTCCCGGTCCTCCCAGCG 3547 Qy 133 CTGGTTTCGACTTCCTGCCCCAGCCACCTCCAGAGAGAGA	193 GCTACTACCGGGGCTGATGACCAATGTGGTTCGTGACCTGACCTCGAGGTGGACCCCCA	Db 3668 CCCTCAAGAGCCTGAAGCAACAACACACCGCAAGCCCTGAAGAGCGCCGCAAGA 3727 Qy 313 ACCCGGCCGACCTGCGAACACCTCAAGATGCCACTCTGAACAGAGAGAG	Qy 373 ACTGGATTGACCCCCAACCAAGGCTGCAACCGGATGCCCATCAAAGTCTTCTGCAACATGG 432 	Qy 433 AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACA 492	Qy 493 TCAGCAAGAACCCCAAGGACAAGAGGATGTCTGGTTCGGCGAGAGCATGACCGATGGTT 552	Qy 553 TCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCTGCCGATGTGGCCATCCAGCTGACCT 612

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90.4%; Pred. No. 3.8e-190;
tive 0; Mismatches 91;
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Publication No. US20060084066A1
GENERAL INFORMATION:
APPLICANT Biogen Idec
TITLE OF INVENTION:
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
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US-10-784-004-826
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Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide capable of self-trimerization which is heterologous to the
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/note= "Glycine repeat region"
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Abr4771
Abr477417
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Aab82454
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         GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                   2443163
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                  2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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AEA28581
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ADD45059
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
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seq sed

Minimum DB Maximum DB

Database

Scoring table:

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score:

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Sequence:

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Run on:

Human

Score

Result No.

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eukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their naturally occurring trimeric ligands. The current sequence is that of the human collagen alpha(1) C-propebtide TO construct protein of the invention. The construct includes a partial glycine-repeat triple helical
polypeptide to be trimerized, and introducing the construct into
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Sequence 311 AA;

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                                                                                                                                                                     YWIDPNOGCNIDAIKVFCNMETGETCVYPTOPSVAOKNWYISKNPKDKRHVWFGESMTDG 180
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                                                                       RSNGLPGP1GPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGPDFSFLPQPPGEKAHDGG
                                                                                                               61 RYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE
                                                                                                                               RYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE
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100.0%; Score 1707; DB 9; Length 311; 100.0%; Pred. No. 6.4e-135;
                           Indels
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                             Matches 311; Conservative
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AEA28581 standard; protein; 699 AA. 28-JUL-2005 AEA28581; RESULT

protein secretion; fusion protein; protein activation; collagen I; CD4 Human soluble CD4-collagen alpha(I) C-propeptide TO fusion protein. (first entry) Homo sapiens. Synthetic.

391. ,427 /label= Human collagen alpha(I) glycine repeat region Key Region

Location/Qualifiers

Chimeric.

WO2005047850-A2

26-MAY-2005.

04-OCT-2004; 2004WO-US032753

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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide expable of self-trimerization which is heterologous to the first polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of culy the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much cathonally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of cuseful for generating as secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their current sequence is that of the human soluble CD4-human collagen alpha(1) C-propeptide to fusion protein (SD4-TO) of the invention. The collagen To construct includes a partial
                                                                                                                                                                        Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
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                                                                                                                                                                                                                                                                              Claim 16; SEQ ID NO 14; 47pp; English.
02-OCT-2003; 2003US-00677877.
                                       (GENH-) GENHUNTER CORP
                                                                                                                    2005-386406/39.
                                                                                                                                       N-PSDB; AEA28580
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                                                                           Liang P; 🥇
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508 180 568 240 300 509 YWIDDWQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDG 389 RSNGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGG RYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE 449 RYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE 121 YWIDPNOGCNLDAIKVFCNMETGETCVYPTOPSVAQKNWYISKNPKDKRHVWFGESMTDG FOFEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGS NEIBIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQE 1 RSNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGG AEA28573 standard; protein; 819 AA. FGFDVGPVCFL 311 FGPDVGPVCFL 699 241 301 AEA28573 ID AEA2 XX RESULT ઠે 셤 ð

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240 748

180 688

RYYRADDANVVRDRDLBVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE

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YWIDPNGGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDG

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301 809

NEIBIRAEGNSRPTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQE 300

POFEYGGOGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGS

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Human alkaline phosphatase-collagen alpha(I) C-propeptide fusion protein.
                                                                                                                                                                                                                                                                 Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 propeptide TO fusion protein (AP-TO) of the invention. The collagen TO construct includes a partial glycine-repeat triple helical region.
                                                                                                                   511. .548 // Alabel= Human collagen alpha(I) glycine repeat region
                                                 protein secretion; fusion protein; protein activation; collagen I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1707; DB 9; Length 819; 100.0%; Pred. No. 2.4e-134;
                                                                                                                                                                                                                                                                                                                    Claim 17; SEQ ID NO 6; 47pp; English.
                                                                                                            Location/Qualifiers
                                                                                                                                                                                               02-OCT-2003; 2003US-00677877.
                                                          Alkaline phosphatase; enzyme
                                                                                                                                                                               04-OCT-2004; 2004WO-US032753
                (first entry)
                                                                                                                                                                                                               (GENH-) GENHUNTER CORP.
                                                                                                                                                                                                                                                2005-386406/39.
                                                                                                                                                                                                                                                         N-PSDB; AEA28572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 819 AA;
                                                                                                                                              WO2005047850-A2.
                28-JUL-2005
                                                                          Homo sapiens
                                                                                                                                                              26-MAY-2005.
                                                                                  Synthetic.
Chimeric.
AEA28573;
                                                                                                                                                                                                                               Liang P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                    Region
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Human soluble TNF-RII-collagen alpha(I) C-propeptide TO fusion protein.

AEA28577 standard; protein; 566 AA.

RESULT 4 AEA28577

FGFDVGPVCFL 311

28-JUL-2005 (first entry)

AEA28577;

protein secretion; fusion protein; protein activation; collagen I; Tumor necrosis factor; TNF-RII.

259. .294 //label= Human collagen alpha(I) glycine repeat region

Location/Qualifiers

Homo sapiens. Synthetic.

Chimeric.

Key Region

04-OCT-2004; 2004WO-US032753 02-OCT-2003; 2003US-00677877

WO2005047850-A2

26-MAY-2005

(GENH-) GENHUNTER CORP.

WPI; 2005-386406/39.

Liang P;

The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, which in turn is solved in-frame to a polypeptide to be trimerized, and introducing the construct into a eukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of enly the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized. Claim 15; SEQ ID NO 10; 47pp; English. N-PSDB; AEA28576.

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Gaps

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Indels

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0; Mismatches

Matches 311; Conservative

Similarity

Best Local

RYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE 120

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1 RSNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGG

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higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for maturally occurring trimeric ligands. The current sequence is their naturally occurring trimeric ligands. The current sequence is that of the human soluble TNF-RII-human collagen alpha(I) C-propeptide TO fusion protein (sTNF-RII-human collagen alpha(I) C-propeptide TO fusion includes a partial glycine-repeat triple helical region.
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Pred. No. 3.8e-134;
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Matches 310; Conservative
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N-PSDB; ADS97949.
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The invention relates to a novel isolated polynuclectide comprising any of the 235 nucleotide sequences described in the specification. The invention further comprises: an isolated polynucleotide encoding a polypeptide with biological activity, where the polynucleotide hybridizes to one of the 235 novel polynucleotides under stringent hybridization convel polynucleotide; an vector comprising a novel polynucleotide; an capture of a vector comprising a novel polynucleotide; and expression vector comprising the novel polynucleotide; which can be operatively associated with a regulatory sequence intermedulates capturession of the polynucleotide in the host cell; an isolated comprising the novel polynucleotide, which can be obtained associated by the novel polynucleotide, or a polynucleotide of hybridizing under stringent conditions to the novel polynucleotide; an expression of the polypeptide and a carrier; an antibody directed against the polypeptide and a carrier; an antibody directed against the polypeptide; a method for identifying a compound that binds to the polypeptide; a method for identifying a compound that binds to the polypeptide; a method for identifying a compound that binds to the polypeptide; a method for identifying a compound that binds in the comprising any of the 235 amino acid sequences described in the conficiention; and a collection of polynucleotides comprising of at least one of the polynucleotides cited above. The polypeptides and antimicrobial activities The novel polynucleotide and antimical and activities the novel polynucleotide may be used to treat attimication.
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New polynucleotides encoding a polypeptide with biological activity, useful for treating inflammation, leukemias, nervous system disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders by gene therapy. The polypeptides and polymucleotides are useful for treating inflammation, leukaemias, nervous system disorders, or infections. This sequence represents one of the 235 novel isolated polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        976 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPGBKAHDGGRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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                                                                                                Claim 20; SEQ ID NO 448; 253pp; English.
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Matches 309; Conservative
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                                                   infections
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Sequence 1464 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the pro-alpha-1 chain of human type I procollagen. The present invention relates to antisense oligomocleotides (ASOs) and their use in inhibiting expression of type I procollagen. The ASOs comprise 18-25 nucleotides and are complementary to a specific region within the type I collagen pro-alpha-1 chain gene (see AAP90491), especially those given in AAP90492-503. They are capable of inhibiting the expression of the pro-alpha-1 chain in a cell that expresses it. The ASOs are used in a claimed method of treating, or reducing a risk of, a collagen disorders may include those caused by overproduction of collagen fibres, such as liver cirrhosis, kidney, liver and heart fibrosis, scleroderma, hypertrophic scars and keloids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antisense DNA oligonucleotide useful for inhibiting the of wild type COLIA1 gene, for treating, reducing the risk of, preventing collagen disorders.
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Human pro-alpha-1 chain of type I procollagen.
                               COLIAl gene; collagen; procollagen; human.
                                                                                                           1. .22
/label= Signal_peptide
                                                                                                                                            23. .1464
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 21-26; 30pp; English.
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                           12-DEC-2000; 2000WO-GB004741.
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UK LTD.
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Matches 309; Conservative
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                                                                                                                                                                                           WO200144455-A2.
                                                                                                                                                                                                                                                                                         15-DEC-1999;
                                                                 Homo sapiens
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necangiogenesis in subjects bearing a vascularised tumour. polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB92075-ABB92141 and ABB90713-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL92046-ABL92041 and ABB92191; normal endothelial markers (NEM) ABL92042-ABL92074, and pan-endothelial markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                         Human, mouse, rat, TEM, tumour endothelial marker, NEM, PEM; cytost
normal endothelial marker, pan-endothelial marker, immunostimulant,
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                                                                                                                                                                                                                                                                              Human Tumour Endothelial Marker polypeptide SEQ ID NO 261.
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ABB90764 standard; protein; 1464 AA.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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ABP68610;

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preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New purified human transmembrane protein, designated as tumor endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1336 FEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE
                                                                                                                                                                                                                                                                                                1156 NGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY
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                                                                                                                                                                         Length 1464;
                                                                                                                                                                                                                 Indels
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                                                                                                                                                                       99.5%; Score 1698; DB 5;
100.0%; Pred. No. 3e-133;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour endothelial marker TEM 38.
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Matches 309; Conservative
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N-PSDB; ABX72044.
                                                                                                                                    Sequence 1464 AA;
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                                                                                                                                                                                                 The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-ABP66637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and
                              IDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNMYISKNPKDKRHVWFGESMTDGFQ 1335
                                                                                                                  FEYGGGGSDPADVAIQLTFLRLMSTRASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and pancreatic tumor polypeptides, useful idiagnosing, preventing and/or treating cancer, particularly pancreatic
        1DPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWY1SKNPKDKRHVWFGESMTDGFQ
                                                                                        FEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE
                                                                                                                                                                           IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 159; 300pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatic cancer expressed protein SEQ ID NO 159
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; 2001US-0305484P.
; 2001US-0313999P.
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31-JAN-2001; 2001US-0265682P.
09-PEB-2001; 2001US-026568P.
21-MAR-2001; 2001US-028561P.
28-APR-2001; 2001US-0287112P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; tumour.
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16-MAY-2001;
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                                                                           The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM), normal polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriaais. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                             IDPNQCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 302
marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
                                                                                                                                                                                                                                                                                                                                                 YRADDANVVRDRDLEVDTTLKSLSQQI ENI RSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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                                                                                                                                                                                                                                                       Length 1464;
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                                                                                                                                                                                                                                                      Score 1698; DB 6;
Pred. No. 3e-133;
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                                                                                                                                                                                                                                             99.5%; Scor.
100.0%; Pred. No. co.
                                                         Disclosure; Page 295-297; 374pp; English
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2001US-0301572P.
2001US-0306501P.
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                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                 Similarity
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27-JUN-2001; 2
18-JUL-2001; 2
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1156 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a method for assessing whether a patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breast cancer diagnosis or treatment by comparing the level of expre
of a marker in a patient sample with that in the control non-breast
cancer sample.
                                                                                                                                                                                                                                                                                                        , Glatt K, Hoersh S, Kamatkar S;
Myer V, Wang Y, Xu Y, Zhao X, Meyers F
Pusztai L, Meric F, Sahin A, Mills GB;
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25-SEP-2001; 2001US-0325002P.
05-MAR-2002; 2002US-0362585P.
14-MAY-2002; 2002US-0380391P.
                                                                                                                                                                                                             (MILL-) MILLENIUM PHARM INC
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Hortobagyi GN,
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FDVGPVCFL 1464
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N-PSDB; ACC50108.
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Mertens M,
Bast RC, Hc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I) agiven in ABR92047 to ABR92164. A higher level of expression of (I) than normal indicates the presence of cervical cancer. Also described: (I) a vector (II) containing (I); (2) a host cell (III) containing (I); (1); and sassessing (MI) whether a patient is afflicted with cervical cancer, comprising comparing the level of expression of a marker in a patient's sample, and the normal level of expression of the marker in a control noregression of the marker in the patient's sample is an indication that the patient safflicted with control sample is an indication that the patient is afflicted with the relative to that in the control sample is an indication that the patient is afflicted with the relative to that in the patient and in vectimes (I) has cytostatic activity, and can be used in gene therapy and in vectimes (I) is useful in detecting, characterising, preventing and treating human cervical cancers. (I) may also be used in verticus prognostic and diagnostic assays, pharmacogenomics and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPSPAGPDPSFLPQPPQEKAHDGGRY 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
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                    cancer; cervical cancer marker; cancer therapy;
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                                                                                                                                                                                                                                                                                                                                                                                       Glatt K, Hoersch S;
                                   detection; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                  Zhao X,
                                                                                                                                                                                                                                        13-JUN-2001; 2001US-0298155P.
13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
                                                                                                                                                                                                    12-JUN-2002; 2002WO-US018638
                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
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                    Human; cervical
                                                                                                                     WO2002101075-A2
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                                                                               Homo sapiens
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The present invention describes a predictor set comprising a plurality of polyuucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase crivity or members of the protein tyrosine kinase cutivity or members of the protein tyrosine kinase comparations the activity of cells, comprising obtaining a sample of cells, comprising obtaining a sample of cells, comprising the activity of the cells express a plurality of markers, and determining whether the cells express a plurality of meathers, and correlating the expression of the markers to the compound's ability to correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polynucleotides and correlates with a disease state; and (3) identifying polynucleotides and disease that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell innes to one or more compounds sensitivity or resistance of cells associated with a disease state, compromed sensitivity or cell innes to one or more compounds, analysing the expression pattern of the microarray. The polynucleotides and polypeptides that predict the sensitivity or censtance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides are useful in predicting the cativity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized cancer; based on patient response at a molecular level. The present conserved the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                 protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein
                                                                                                                                                                                                                                                                                                             predictor set; protein tyrosine kinase activity modulator;
                                                                                                                                                                                                                                                                  Human src biomarker polypeptide SEQ ID NO:331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shaw P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; SEQ ID NO 331; 139pp; English.
                                                                                                                                   ADD14142 standard; protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee FY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2003; 2003WO-US001981.
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                                                                                                                                                                                                                       (first entry)
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1456 FDVGPVCFL 1464
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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Length 1464;

99.5%; Score 1698; DB 7; 100.0%; Pred. No. 3e-133;

Best Local Similarity

Query Match

Sequence 1464 AA;

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1215
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                                                                                         YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease, arthritide, gene expression analysis;
rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
antiarthritic, osteopathic; antigout; antiinflammatory; dermatological;
immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease
                                               IDPNOGCNLDAIKVFCNMETGETCVYPTOPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ
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                              NGLPGPIGPPGPRGRICDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY
 Gaps
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 Mismatches
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 Conservative
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                                                                                                                                                                                                                                                                                                                                          311
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GENBANK; NP_000079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; acreening the efficacy of a candidate drug in vitro for the treatment of collageninduced arthritis; and reducing the symptoms associated with collageninduced arthritis. The compositions of the invention have the following
                                                                                                                                                                                                activities: Immunosupressive, antirheumatic, antiarthritic, osteopathic, antigout, antinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease a rathritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEYGGOGSDPADVAIQLTFLRLMSTEASONITYHCKNSVAYMDQQTGNLKKALLLKGSNE 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Match 99.5%; Score 1698; DB 7;
Local Similarity 100.0%; Pred. No. 3e-133;
168 309; Conservative 0; Mismatches 0;
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                                                                                                                                                                                     The invention relates to a novel method for detecting soft tissue sarcoma
                                                                                                                                                                                            which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarched of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic sacid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma—upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                 Early detection of soft tissue sarcoma comprises determining expression
                                                                                                             of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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0; Mismatches
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                        (PROT-) PROTEIN DESIGN LABS INC.
 26-NOV-2002; 2002US-0429739P
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Matches 309; Conservative
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                                                                                                                                                                                                                                                                                                           Myerow SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises a method for diagnosing colon cancer in an individual, the method involves obtaining a serum sample from the individual and detecting the presence of either TIMBLO R Regi-alpha and an additional colorectal cancer-associated marker. The method of the invention is useful for diagnosing colon cancer in an individual. The present amino acid sequence represents a human colorectal cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1216 YRADDANVYRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing colon cancer in individual, preferably human, by detecting presence of TIMP 1 in sample, where presence of TIMP 1 in sample is indicative of colon cancer in individual.
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(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
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Johnson KA,
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Brown-Shimer SLA, Thiagalingam A,
                                                                                                                                           13-DEC-2002; 2002US-0433554P.
                                                                                            15-DEC-2003; 2003EP-00257868
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- protein search, using sw model OM protein Run on:

April 26, 2006, 16:14:30 ; Search time 28.4247 Seconds (without alignments) 1052.725 Million cell updates/sec

US-10-677-877A-2

1707 1 RSNGLPGPIGPPGPRGRTGD......LDVGAPDQEFGFDVGFVCFL 311 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283416 segs, 96216763 residues Searched:

of hits satisfying chosen parameters: Total number

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 80:* Database

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1-369,'L',371-589 <DAL>

A;Cross-references: UNIPROT:014992; UNIPROT:016053; UNIPROT:013896; UNIPROT:013996; UNIPROT:0139996; UNIPROT:0139992; UNIPROT:0139992; UNID:0139992; UNID:0139992; UNID:0139992; UNID:0139992; UNID:0139992; UNID:013999220

A; Molecule type: DNA A; Mesidues: 1-58, Q', 60-181 < CHU> A; Residues: 1-58, Q', 60-181 < CHU> A; Cross-references: UNIPARC: UPIO000173B3C; EMBL: X00820; NID: 935657; PIDN: CAA25394.1; PID R; Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.-, C. Balol. Chem. 262, 15151-15157, 1397 A; Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh-A; Reference number: 155254; MUID: 88033098; PMID: 2822714

A;Status: translation not shown; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-45 <ROS> A; Accession: I55254

A;Cross-references: UNIPARC:UPI000016A6B2; GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E. Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987 A;Title: Regulatory elements in the first intron contribute to transcriptional control of A;Reference number: A39943; MUID:88097389; PMID:3480516

A;Wolecule type: DNA A;Residues 1.34 ÷BOR> A;Cross=references: UNIPARC:UPI000016A6B1; GB:J03559; NID:g180876; PIDN:AAAS2052.1; PID:ç R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A;Molecule type: mRNA
A;Residues: 1179-1336,1339-1464 <CH6>
A;Cross-references: UNIPARC:UP1000017384E
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                                                                                                                                                                                                                      A;Accession: 152905
A;Status: translated from GB/EMBL/DDBJ
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J. Biol. Chem. 260, 2315-2320, 1985

A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter 8 A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter 8 A;Reference number: I55237; MUID:85130970; PMID:2857713

A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Resadues: 1-34 <CH2>
A;Cross-references: UNIPARC:UPI000016A6B1; GB:M10627; NID:g180383; PIDN:AAA51992.1; PID: R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist A;Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-termina rome, type VII.
A;Reference number: A35233; MUID:90202908; PMID:2318855
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A;Cross-references: UNIPARC:UPI0000173844; UNIPARC:UPI0000173845; UNIPARC:UPI0000173846; R;Wittz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N. Connect. Tissue Res. 29, 1-11, 1993
A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of the A;Reference number: I52905; MUID:93339042; PMID:8339541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 342-352,'C',354-359 <WI2>
A;Cross-references: UNIPARC:UPI0000070EE6; GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:
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A; Residues: 425-1250, X, 1252-1328, S, 1330-1390, XX, 1392-1464 <BER>
A; Residues: 425-1250, X, 1252-1328, S, 1330-1390, XX, 1392-1464 <BER>
A; Cross-references: UNIPARC: UP10000173B4A, GB: K01228; NID:g180391; PIDN: AAA51995.1; PID: £
A; Note: sequence partially completed for missing nucleotides by A29439
R; Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
Biol. Chem. 260, 691-694, 198
A; Title: Whitiexon deletion in an osteogenesis imperfecta variant with increased type IIII
A; Reference number: A22161; WUID: 85104934; PMID: 2981843
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A,Residues: 472-594, R.,596-607 <CH3>
A,Residues: 472-594, R., 191000011F796; GB:K03178; GB:K03179; NID:G179612; NID:G179612
A,Note: the authors translated the codon CGT for residue 595 as Pro
A;Nallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
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A; Residues: 710-720, FE', 722-737, FE', 739-745 < WAL>
A; Cross-recences: UNIPARC:UP1000017384B
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R; Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
R; Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
A; Ference number: 3, 2201-2206, 1994
A; Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the Cs
A; Reference number: 154365, MUD:95187161; PMID:7881420
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A; Residues: 746-766, 'S', 768-781 < PCOR.
A; Residues: 746-766, 'S', 768-781 < PCOR.
A; Residues: 746-766, 'S', 768-781 < PCOR.
A; Cross-references: UNIPARC: UP1000016A6FA, GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID
B; Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
J. Biol. Chem. 268, 18218-18225, 1993
A; Fitle: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of typ.
A; Reference number: A47426; MUID:93352646; PMID:8349697
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A;Reaidues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: UNIPARC:UPI0000073A2A; GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:c
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different mutana, A;Accession: B47426
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A; Title: Nuclectide sequences of complementary deoxyribonucleic acids for the proalphal A; Reference number: A90476; MUID: 84080385; PMID: 6689127
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
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A;Experimental source: normal dermal fibroblast culture
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A;Accession: A35336
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A; Molecule type: DNA
A; Residues: 1442-1453 < MRT>
A; Residues: 1442-1453 < MRT>
A; Residues: 1442-1453 < MRT>
A; Cross-references: UNIPARC:UP1000000691; EMBL:XS7981; NID:g50484; PIDN:CAA41046.1; PID
B; French, B.T.; Lee, W.H.; Maul, G.G.
Gene 39, 311-312, 1985
A; Title: Nucleotide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A; Reference number: A23982; MUID:86137403; PMID:3841523
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A;Residues: 518-1128 <FRE>
A;Cross-references: UNIPARC:UPI000016CC46; GB:M14423; NID:9192261; PIDN:AAA37333.1; PID:
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A;Molecule type: DNA
A;Residues: 735-1130 <RES>
A;Cross-references: UNIPARC:UP1000016CC47; GB:M17491; NID:9192263; PIDN:AAA37334.1; PID:
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A; Residues: 1-80,'E',82-105,'D',107-185;1031-1201,'G',1203-1218,'E',1220-1221,'T',1223-13
A; Residues: 1-80,'E', 82-105,'D',107-185;1031-1201,'G',1203-1218,'E',1220-1221,'T',1223-13
A; Cross-references: UNIPARC:UPI0000E6565; UNIPARC:UPI00017738A
B; Rhodes, K.; Rippe, R.A.; Umexa, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
Mol. Cell. Biol. 14, 5950-5960, 1994
A; Title: DNA methylation represses the murine alpha 1(I) collagen promoter by an indirect A; Reference number: 148300; MUID:94344105; PMID:8065328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen alpha 1(I) chain precursor - mouse (Species: Mus musculus (house mouse) (C.Species: Mus musculus (house mouse) (C.Species: Mus musculus (house mouse) (C.Space: 13-Jan-1995 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 (C.Accession: S57243; S16374; A23982; 149559; 149557; S39789; 148300; S21626 R;Li, S.W.; Khillan, J.; Prockop, D.J. Matrix Biol. 14, 593-595, 1994 (Matrix Biol. 14, 593-595, 1994 A;Title: The complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of type I) A;Reference number: S57243
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Mol. Cell. Biol. 2, 1362-1371, 1982
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Mol. Cell. Biol. 2
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Proc. Natl. Acad. Sci. U.S.A. 81, 1504-1508, 1984
A;Title: Insertion of retrovirus into the first intron of alphal(I) collagen gene least reference number: 149557; MUID:84170331; PMID:6324198
A;Accession: 149557; MUID:84170331; PMID:6324198
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-25 - RE2.
A;Crosserseferences: UNIPARC:UPI00000E5879; GB:K01689; NID:g192246; PIDN:AAA37330.1; Biochim. Biophys. Acta 1216, 469-474, 1993
A;Title: Genomic sequence of mouse COLIA1 encoding the collagen propeptides.
A;Reference number: S39789; MUID:94092741; PMID:8268229
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                                                                                                                                                                                                                    PEYGGEGSNPADVAIQLTFLRLMSTEATQNVTYHCKNSVAYMDHDTGNLKKALLLQGANE 404
                                                                                                                                                                  IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG
303 FDVGPVCFL 311
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IDIGPVCFL 473
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C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
P;244-473/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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150629
collagen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-8ep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150629
R;Puller, F; Boedtker, H.
Biochemistry 20, 996-1006, 1981
A;Title: Sequence determination and analysis of the 3' region of chicken pro-alpha 1(1)
A;Reference number: 150623; MJD:81160715; PMID:6927845
A;Accession: 150629
A;Accession: T50629
A;Accession: 
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                                       A.Accession: E47426
A.Molecule type: mRNA
A.Residues: 1179-1387, K',1389-1464 <CH7>
A.Facsidues: 1179-1387, K',1389-1464 <CH7>
A.F.Cross-references: UNIPARC:UPI000017384F
A.Experimental source: fetal cell 88-251
R;Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.;
J. Biol. Chem. 263, 14605-14607, 1988
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Pred. No. 8.4e-117;
3; Mismatches 0;
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fetal cell 86-146
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99.0%;
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Best Local Similarity 99.0
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A; Experimental source:
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Biochem. J. 285, 287-294, 1992
A;Title: Structural analysis of the regulatory elements
A;Reference number: S24270; MUID:92344585; PMID:1637314
A;Accession: S24270
                                                                                                                                                                                                                                A;Status: translation not shown
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NyAlternate names: procollagen alpha 1(II) chain
NyAlternate names: procollagen alpha 1(II) chain
NyAlternate names: procollagen alpha 1(II) chain
NyContains: chondrocalcin; collagen alpha 1(II) chain
CyBecies: Homo aspiens (man)
CyBecies: Any-1986 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
CyAccession: A38513; 806715; 524270; A4828; 806496; A35428; A30147; A33116; 864674; 863
7250; 137251; 137252; 137253; 137254; 155338; 159535; 161910
R;Ryan, M.C.; Sieraski, M.; Sandell, L.J.
R;Ryan, M.C.; Sieraski, M.; Sandell, L.J.
Ayitle: The human type II procollagen gene: identification of an additional protein-cod
A;Reference number: A38513
A;Accession: A38513
A;Accession: A38513
A;Molecule type: DNA
A;Residues: 1-103 < RXA>
A;Residues: 1-103 < RXA>
A;Cose_references: UNIPROT:P02458; UNIPROT:Q14042; UNIPROT:Q16672; UNIPROT:Q12985; UNIF
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Risu, M.W.; Lee, B.; Ramirez, F.; Machado, M.; Horton, W.

Nucleic Acids Res. 17, 9473, 1989

A;Title: Nucleotide sequence of the full length cDNA encoding for human type II procolla A;Reference number: S06715; MUD: 90067946; PMID: 2587267

A;Accession: S06715

A;Accessio
                                                                          A;Molecule type: DNA
A;Residues: 1-80,'E',82-105,'D',107-147 <REF>
A;Cross-references: UNIPARC:UP1000017738B; EMBL:X54876; NID:g50486; PIDN:CAA38657.1; PID
                                                                                                                                                                                                                                                                                                                           Ajdene: COLIAI
Ajntrona: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/
Ajntrona: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/
Ajntrona: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 95/3; 1004/3; 1004/3; 1002/3; 1058/
C; Superfamily: collagen alpha 1(1) chain matrix; glycoprotein; heterotrimer; triple helix; F;1-22/Domain: signal sequence #status predicted <SIG.
F;30-81/Domain: amino-terminal propeptide #status predicted <PRO>
F;30-89/Domain: von Willebrand factor type C repeat homology <WC>
F;152-1453/Product: collagen alpha 1(1) chain #status predicted <WAT>
F;1224-1453/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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1445 LDIGPACEV 1453
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A;Accession: A24828
A;Molecule type: DNA
A;Roslaus: 1-8, T',10-28 <NUN>
A;Cross-treferences: UNIPARC:UPI000016A71A, GB:M25698; NID:g180872; PIDN:AAA52051.1; PID:g
R;Baldwin, C.T.; Reginato, A.M.; Smith, C.; Jimenez, S.A.; Prockop, D.J.
Biochem, J. 262, 521-528, 1989
A;Title: Structure of cDNA clones coding for human type II procollagen. The alpha-1(II) c
A;Reference number: S06496; MUID:90026318; PMID:2803268
A;Accession: S06496.
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A; Residues: 7-28, "R', 99-157, 'P', 159-440, 'G', 442-456, 'E', 458-640, 'A', 642-831, 'PA', 834, 'F',
A; Residues: 7-28, "R', 99-157, 'P', 159-440, 'G', 442-456, 'E', 458-640, 'A', 642-831, 'PA', 834, 'F',
A; Residues: 7-28, "R', 99-157, 'P', 159-440, 'G', 442-456, 'E', 458-640, 'A', 642-831, 'PD:
A; Note: alternative splice form 1
B; Ryan, M.C.; Sandell L.J.
B; Ryan, M.C.; Sandell L.J.
B; Ryan, M.C.; Sandell L.J.
A; Title: Differential expression of a cysteine-rich domain in the amino-terminal propeption A; Title: Differential expression of a cysteine-rich domain in the amino-terminal propeption A; Reference number: A35428; MUD: 90285153; PMID: 2355003
A; Title: Differential expression of a cysteine-rich domain in the amino-terminal propeption A; Status: not compared with conceptual translation
A; Reference number: UNIPARC: UPI0000173B66
A; Molecule type: mRNA
A; Cross-references: UNIPARC: UPI0000173B66
A; Note: alternative splice form 2; splicing appears to be under developmental regulation R; Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F.
Genomics 4, 438-441, 1989
A; Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide confine A; Reference number: A30147; MUD: 89233138; PMID: 2714801
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A, Residues: 171-172, 'C', 174-175 <ALA>
A, Residues: 171-172, 'C', 174-175 <ALA>
A, Residues: 171-172, 'C', 174-175 <ALA>
A, Note: mutant sequence from a family with family with primary generalized osteoarthritis
R, Diab, M.; Mu, J.J.; Eyre, D.R.
Blochem W. 314, 327-332, 1996
A, Fitle: Collagen type IX from human cartilage: a structural profile of intermolecular collagentype IX from human cartilages. A; Reference number: 864673; MUID:96195147; PMID:8660302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S64674
A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: UNIPARC:UD10000173B69; UNIPARC:UD10000173B6A
A;Cross-references: UNIPARC:UD10000173B69; UNIPARC:UD10000173B6A
R;Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, I
R;Franc, S.; Marzin, E.34, 125-131, 1995
A;Friel: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil cart
A;Reference number: S63514; MUID:96096730; PMID:8529631
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A;Molecule type: protein
A;Reaidues: 243-2561;575-261;775-779 <FRA>
A;Reaidues: 243-2561;575-261;775-761;765-779 <FRA>
A;Cross-references: UNIPARC:UP10000173B6B; UNIPARC:UP10000173B6D
B;Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, A;Tiller, G.E.; Meis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, A;Tiller, B, NRA-splicing mutation (G+FIVS20) in the type II collagen gene (COL2A1) in a A;Reference number: 138867; MUID:95150028; PMID:7847372
of the type-II procollagen gene.
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A;Molecule type: DNA
A;Residues: 104-157, P., 159-236 <SUM>A;Residues: 104-157, P., 159-236 <SUM>A;Residues: 104-157, P., 159-236 <SUM>A;Residues: 104-157, P., 159-236 <SUM>A;Residues: 104-157, P., 159-236 <SUM
B;Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
B;Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
A;Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
A;Alitle: Single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1) and a single base mutation in the type II procollagen gene (COL2A1) as a cause of principal and a single base mutation in the type II procollagen gene (COL2A1)
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A; Residues: 1-28 «VIX»
A; Residues: 1-28 «VIX»
A; Residues: 1-28 «VIX»
A; Note: this translation is not annotated in GenBank entry HSPROCOE1, release 111.0
R; Nunez, A.M.; Kohno, K.; Martin, G.R.; Yamada, Y.
Gene 44, 11-16, 1986
A; Title: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A; Reference number: A24828; MUID:87031574; PMID:3021582
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PIDN: C

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A)Cross-references: UNIPARC:UP10000173B73; GB:M12048; NID:g180017
A)Note: this translation is not annotated in GenBank entry HUMCT12A, release 111.0
A;Note: the codons given for 133-Lys (AGG) and 1350-G1y (GCA) are inconsistent with the R;Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez, M.Uclèic Acids Res. 13, 2207-2225, 1985
A;Title: Isolation and partial characterization of the entire human pro alpha 1(II) coll A;Reference number: 137249; MUID:85215609; PMID:2987845
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submitted to the EMBL Data Library, June 1996
A;Description: Cloning of equine type II collagen and modulation of its expression in eq
                                                                                                                                                                                                                   A,Cross-references: UNIPARC:UP1000006EA4D; GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g Knuncz, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y. Bicohemistry 24, 6348, 1985
Bicohemistry 24, 6343-6348, 1985
A,Title: Isolation and partial characterization of genomic clones coding for a human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 7-28;'R', 99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-1
A;Cross-references: UNIPARC:UP10000071780; UNIPARC:UP10000173B74; UNIPARC:UP10000173B75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPARC:UP10000071780; UNIPARC:UP10000173B74; UNIPARC:UP10000173B75;
                                                        A;Cross-references: UNIPARC:UP1000016A61A; EMBL:X00339; EMBL:X00298; NID:g334699;
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N;Alternate names: type II collagen
C;Species: Bquus caballus (domestic horse)
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45467
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A;Note: the GenBank PID is based on an incorrect reading frame
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                                                                                          A;Accession: B21733
A;Molecule type: DNA
A;Residues: 894-909,'PE' <STR2>
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Matches 213; Conservative
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EFGVDIGPVCFL 1487
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                 <STR1>
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A; Residues: 1296-1358 <NUN2>
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                 1245-1295
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 440,'G', 442-456,'E', 458-480,'P', 482-509 <TILL>
A;Cross-references: WIPPARC:UPI000006F3AF; EMBL:U15195; NID:g557053; PIDN:AAB60370.1; PI
R;Ramirez, F.
R;Ramirez, F.
R;Ramirez, F.
R;Ramirez, F.
A;Reference number: S04892
A;Reference number: S04892
A;Accession: S04892
A;Cross-references: UNIPARC:UPI000016A700; EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PIE
FEBS Lett. 250, 171-174, 1989
A;Title: Structural analyses of the polymorphic area in type II collagen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPARC:UPI0000173B6E; EMBL:X16158; NID:g29951; PIDN:CAA34278.1; PID A34282.1; PIDS:J35022; PIDN:CAA4283.1; PID:g1335024
R,34282.1; PID:g1335022; PIDN:CAA4283.1; PID:g1335024
R,5809aert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, I J. Biol. Chem. 267, 22522-22526, 1992
J. Biol. Chem. 267, 22522-22526, 1992
J. Shiller, An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain pro A;Reference number: A44309; MUID:93054548; PMID:1429602
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A; Residues: 752-831, 'PA', 834, 'F', 836-1005, 'K', 1007-1036,'Q', 1038-1052,'E', 1054-1068,'T',
A; Residues: 752-831, 'PA', 834, 'F', 836-1005, 'K', 1007-1036,'Q', 1038-1052,'E', 1054-1068,'T',
A; Crose: references: UNIPARC:UPI000017386F; GB:L00977; NDISG180812; FIDN:AAB23914.1; PID:
A; Note: requence extracted from NCBI backbone (NCBIP:117273); parts of this sequence wer
A; Note: mutant sequence associated with perinatal lethal hypochondrogenesis
A; Note: mutant sequence associated with perinatal lethal hypochondrogenesis
A; Note: Main, D.L.; Murzay, L.W.; Cohn, D.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3889-3893, 1990
A; Title: Tandem duplication within a type II collagen gene (COL2A1) exon in an individua
A; Reference number: $16502; MUID:90251662; PMID:2339128
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A; Residues: 1164-1184, GPSGKDGANGIPGPI', 1185-1199 <TILL2>
A; Residues: 1164-1184, GPSGKDGANGIPGPI', 1185-1199 <TILL2>
A; Cross-references: UNIPARC: UPIO00011F7F2; EMBL: M37126; NID: g180808; PIDN: AAA52037.1; PI
A; Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R; Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
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A; Title: Identification and characterization of the human type II collagen gene (COL2A1)
A; Reference number: A02858; MUID: 85190534; PMID: 3857598
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Mucleic Acids Res. 12, 1025-1038, 1984
A;Title: Isolation and characterization of genomic clones corresponding to the human typ
A;Reference number: A21733; MUID:84118798; PMID:6320112
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A;Residues: YEV, 1244-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 <VAN>
A;Cross-references: UNIPARC:UPI0000173B70; UNIPARC:UPI0000173B71; UNIPARC:UPI0000173B72
A;Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prof
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A; Molecule type: DNA
A; Residues: 1032-1056, N', 1058-1068, 'T', 1070-1487 < CHE>
A; Residues: 1032-1056, N', 1058-1060016A6BB; GB: J00116; NID: g180395; PIDN: AAA51997.1; PID: R; Elima, K.; Vuorio, T.; Vuorio, E.
R; Elima, K.; Vuorio, T.; Vuorio, E.
A; Elima, K.; Vuorio, T.; Vuorio, E.
A; Fille: Determination of the single polyadenylation site of the human pro-alpha-1(II) c
A; Reference number: A27280; MUID: 88067771; PMID: 2825137
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A;Residues: 1175-1487 <ELL>
A;Cross-references: UNIPARC: UPIO00016A71B; EMBL:X06268; NID:g30096
A;Experimental source: fetal epiphyseal cartilage
R;van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Biochem. J. 237, 923-925, 1986
A;Title: Chondrocalcin is identical with the C-propeptide of type
A;Reference number: A57033; MUID:87099927; PMID:3800925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S05000
A;Molecule type: DNA
A;Residues: 630-640,'A',642-785 <VIK2>
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Collage alpha 1(II) chain precursor (long splice form) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 31-Dec-2004
C;Accession: B41182
C;Accession: B41182
J. Biol. Chem. 266, 16862-16869, 1991
A;Fitle: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and & A;Recession: B41182
A;Recession: B41182
A;Recession: B41182
A;Recession: B41182
A;Recession: B41182
A;Residues: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1487 <AMET-
A;Cross-references: UNIFROT:062031; UNIPROT:062032; UNIPROT:062033; UNIPROT:062033; UNIPROT:062033; UNIPROT:062033; UNIPROT:062033; UNIPROT:062033; UNIPROT:0f20000177378
C;Superfamily: fibrillar collagen carboxyl-terminal homology; von Willebrand factor type
C;Reywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime:
F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>
F;1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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                                                                                                     120 EYWIDPNOGCNLDAIKVPCNMETGETCVYPTQPSVAQXWWYISKNPKDKRHVWFGESMTD 179
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                            61 RYYRADDA-NVYRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSG
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70.7%; Score 1206.5; DB
Best Local Similarity 67.6%; Pred. No. 3.7e-81.
Matches 211; Conservative 45; Mismatches 5:
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|408 EFGVDIGPVCFL 1419
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A41182
collagen alpha 1(II) chain precursor - mouse
collagen alpha 1(II) chain by a four collagen mouse)
Cjacte: 28-may-1992 #sequence_revision 28-may-1992 #text_change 13-Aug-1999
Cjaccession: A41182; A44886.
A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Residues: 1-419 cMET-
A;Cross-references: UNIPARC:UPIO000177381; GB:M65161
R;Cheah, K.S.; Lau, B.T.; Au, P.K.; Tam, P.P.
Bevelopment 111, 945-933, 1991
A;Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilag A;Reference number: A44885; MUID:91347939; PMID:1879363
A;Reference number: A44885
A;Residues: 1-28 cGHS-
A;
A; Reference number: 222977
A; Accession: T45467
A; Ascension: T45467
A; Ascension: T45467
A; A; Molecule type: mRNA
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A; Cross-references: UNIPROT: C28396; UNIPARC: UPIO00008834A; EMBL: U62528; PIDN: AAB05773.1
C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
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                                                                                                                                                                                                                                                                        54; Indels
                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                   71.0%; Score 1212.5; DB 2
68.3%; Pred. No. 1.2e-81;
iive 42; Mismatches 54;
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llarity 67.6%; Pred. No. 3.5e-81;
Conservative 45; Mismatches 53;
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EFGVDIGPVCFL 1418
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                                                                                                                                                                                                                                               Best Local Similarity 68.3
Matches 213; Conservative
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Matches 211;
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collagen alpha 1'(II) chain precursor - African clawed frog
Cispecies: Xenopus laevis (African clawed frog)
Cjoate: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
CjAccession: A40333
R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis emitaterence number: A40333; MUID:92011898; PMID:1918153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1492 cSUA>
A; Residues: 1-1492 cSUA>
A; Residues: 1-1492 cSUA>
A; Cross-references: UNIPROT:091718; UNIPROT:091717; UNIPARC:UPI0000177382; GB:M63596
A; Note: this sequence is presented as substitutions relative to another sequence in a fixes they replace; the appropriate interpretation of the sequence figure was reconstructed c; Superfamily: collagen alpha i(I) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: colled coil; extracellular matrix; glycoprotein; trimer; triple helix F; 37-96/Domain: von Willebrand factor type C repeat homology cVWC>
F; 1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                               1240 PMRYMRADQASSSVIQTADVEANLKTINNQIESIIRSPDGTKKNPARTCRDLKLCHPEWK 1299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 KGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAP 297
                                                                                                                                                                            DGFQFEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLK
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                                                                             GEYWIDPNOGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMT
                                                                                                                                                                                                                                                                      GSNEIBIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPD
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QEFGVDIGPVCFL 1486
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hes 205;
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collagen alpha 1(II) chain precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Bate: 115, 565-575, 1991

A;Risu, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.

J. Cell Biol. 115, 565-575, 1991

A;Ritle: Expression of two nonallelic type II procollagen genes during Xenopus laevis en A;Recenence number: A40333; MUID:92011898; PMID:1918153

A;Accession: B40333

A;Status: preliminary

A;Residues: 1-1486 <SUNA

A;Residues: 1-1486 <SUNA

A;Residues: 1-1486 <SUNA

A;Cross-references: UNIPROT:091718; UNIPROT:091717; UNIPARC:UPI0000173B50; GB:M63595

C;Superfamily: collagen alpha 1(I) rohan; fibrillar collagen carboxyl-terminal homology; C;Reywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix

F;37-96/Domain: von Willebrand factor type C repeat homology <VWC>

F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <</td>
                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:090412; UNIPARC:UPI00000FC847; EMBL:U23822; NID:9773660; PIC C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; F;236-464/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
C;Species: Brachydanio rerio (zebra fish)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S59513
R;Yan, Y; Hotta, K.; Riggleman, B.; Postlethwait, J.H.
submitted to the EMBL Data Library, March 1995
A;Description: Expression of a type II collagen gene in the zebrafish embryonic axis.
A;Reference number: S59513
A;Reference number: S59513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-464 <PAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGRYYRADDA-NVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWK 117
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                                                                                                                                                                                                                                                                                                                                                                   69.0%; Score 1177.5; DB 2; Length
68.2%; Pred. No. 1.2e-79;
ive 37; Mismatches 56; Indels
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DQEFGVDIGAVCFL 464
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Best Local Similarity 66.1
Matches 207; Conservative
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A; Molecule type: DNA
A; Residues: 1-245 < BOES
A; Cross-references: UNIPROT: P02467; UNIPARC: UPI00001712EA; GB: M25963; NID: G211581; PIDN: I)
A; Accession: 150207
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 246-431 < BOES
A; Cross-references: UNIPARC: UPI00001712AA; GB: M25965; NID: G211583; PIDN: AAA69961.1; PID: CROSS-references: UNIPARC: UPI00001712AA; GB: M25965; NID: G211583; PIDN: AAA69961.1; PID: CROSS-references: UNIPARC: UPI00001712AA; GB: M25965; NID: G211583; PIDN: AAA69961.1; PID: CROSS-reference number: S07354; MUID: 84297217; PMID: 6473103
A; Reference number: S07354; MUID: 84297217; PMID: 6473103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI00001712EC; EMBL:X02657; NID:g63314; PIDN:CAA26493.1; PID A;Accession: S10480
A;Accession: S10480
A;Accession: S10480
A;Rolecule type: DNA
A;Residues: 17-73 <TAW>
A;Residues: 17-73 <TAW>
A;Cross-references: UNIPARC:UPI0000173BAD
A;Cross-references: UNIPARC:UPI0000173BAD
A;Cross-references: UNIPARC:UPI0000173BAD
A;Cross-references: UNIPARC:UPI0000173BAD
A;Cross-references: UNIPARC:UPI0000173BAD
A;Cross-references: UNIPARC:UPI0000173BAD
A;Cross-reference type: DNA: Sobel, M.E.; Yamada, Y.; Pastan, I.; de Crombrugghe, B.
A;Title: Structure of the promoter for chicken alpha-2 type I collagen gene.
A;Reference number: S11146; MUID:82060240; PMID:6946474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cross-references: UNIPARC:UPI0000173BAE; EMBL:J00821; Vogeli, G.; Irani, M.; Pastan, Jl. Alamda, Y.; Avvedimento, V.E.; Mudryj, M.; Ohkubo, H.; Vogeli, G.; Irani, M.; Pastan, Jl. Ball 12, 887-892, 1980; The callagen gene: evidence for its evolutinary assembly by amplification of a Il. The callagen gene: evidence for its evolutinary assembly by amplification of a Il. Reference number: IS0170; MUID:81112157; PMID:7460017
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A;Molecule type: DNA
A;Residues: 126-161 <7A2>
A;Cross-references: UNIPARC:UP1000001712A9; GB:J000828; NID:g211295; PIDN:AAA51612.1; PID:
                     C;Accession: I50206; I50207; S07354; S10848; S10480; S11146; I50628; I50170; I50625; I500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-33 - AHO-
A; Residues: 1-32 - AHO-
A; Residues: 1-32 - AHO-
A; Cross-references: UNIPRRC: UDI0000173BAC; EMBL: X00760; NID: 963266; PIDN: CAA25330.1; PID
R; Tate, V.E.; Finer, M.H.; Boedtker, H.; Doty, P.
R; Tate, V.E.; Finer, M.H.; Boedtker, H.; Doty, P.
R; Tate, V.E.; Finer, M.H.; Boedtker, H.; Doty, P.
A; Title: Chick pro-alpha-2 (1) collagen gene: exon location and coding potential for the A; Reference number: S10480; MUID: 83246518; PMID: 6135195
A; A; Accession: S10848
A; A; Residues: 1-89 < TAT>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 126-161 <YAM>
A;Crost-references: UNIPARC:UPI00001712A9; EMBL:V00400; NID:g63305; PID:g833611
A;Accession: 150170
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A;Accession: 150626
A;Status: preliminary; translated from GB/EMBL/DDBJ
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;Cross-references: UNIPARC:UPI0000173BB0; EMBL:V00398; NID:g63299; PID:g833610
                              R;Boedtker, H.; Finer, M.; Aho, S.
Ann. N. Y. Acad. Sci. 460, 85-116, 1985
A;Title: The structure of the chicken alpha 2 collagen g
A;Reference number: ISO206; MUID:86185168; PMID:3868961
A;Accession: ISO206
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A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 530-558 <YA3>
                                                                                                                                                                                                                                                                                 A; Status: translated from GB/EMBL/DDBJ
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A,Molecule type: DNA
A,Residues: 1-15 <VOG>
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collagen alpha 1(II) chain precursor - chicken (fragment)
Cypectes: 3011us gallus (chicken)
Cypectes: 3011us (chicken)
Cypectes: 301us (chicken)
Cypectes: 301us (chicken)
Cypectes: 301us (chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMET 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYGGQGSDPADVAIQLTFL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIRAEGNSRFTYSVTVDGC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239
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CGCH28
collagen alpha 2(I) chain precursor - chicken (fragments)
c;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 24-Apr-1984 #sequence_revision 15-Aug-1997 #text_change 09-Jul-2004
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65.9%; Score 1124.5; DB 1; Length 288;
Best Local Similarity 68.9%; Pred. No. 5.6e-76;
Matches 199; Conservative 37; Mismatches 50; Indels 3;
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A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 433-483 < YA5>

Accession: I50624

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A;Molecule type: DNA
A;Residues: 536-558 <AVV>
A;Cross-references: UNIPARC:UP100001712AD; GB:M10581; NID:g211323; PIDN:AAA48637.1; PID:
A;Cross-references: UNIPARC:UP100001712AD; GB:M2neV, J.; Fuller, F.; Crkvenjakov, R.; Bo
                                                                                                                                                                                                                                                                                                                                                                ;Molecule type: mRNA;
;Residues: 484-505 <LEH>
;Cross-references: UNIPARC:UPI00001712AB; GB:J00837; NID:g4530617; PIDN:AAA51614.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Johnson 24/1; 27/3; 33/3; 45/3; 73/3; 92/3; 107/3; 125/3; 143/3; 161/3; 179/3; 197/3; A; Introns: 24/1; 27/3; 33/3; 45/3; 73/3; 92/3; 107/3; 125/3; 143/3; 161/3; 179/3; 197/3; A;Note: the list of introns is incomplete
A;Note: the list of introns is incomplete
C;Superfamily: ocollagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: blocked amino end; coil-ed coil; extracellular matrix; glycoprotein; hydroxypi
F;12-27/Domain: signal sequence #status predicted <81G>
F;23-77/Domain: amino-terminal propeptide #status predicted <PRO>
F;78-99/Froduct: collagen alpha 2(1) chain (fragments) #status predicted <MATN>
F;78-99/Region: amino-terminal nonhelical telopeptide
F;78-96/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;78/9/Modified site: blocked amino end (GIn) (in mature form) (probably pyrrolidone carbox F;88)/Modified site: allypine (Lys) #status experimental
F;86/Shiding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Gallus gallus (chicken)
C;Species: Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 23-May-1997
C;Accession: S10847; S65690
R;Dickson, L.A.; Ninomiya, Y.; Bernard, M.P.; Pesciotta, D.M.; Parsons, J.; Green, G.; E)
J. Biol. Chem. 256, 8407-8415, 1981
A;Title: The exon/intron structure of the 3'-region of the pro-alpha-2(1) collagen gene.
A;Reference number: S10847; MUID:81264246; PMID:6267043
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A;Note: the authors translated the codon ATA for residue 207 as Asp, AGC for residue 216
                                                                                                                            Richrach, H.; Frischauf, A.M.; Hanahan, D.; Wozney, J.; Fuller, F.; Crkvenjakov, Proc. Natl. Acad. Sci. U.S.A. 75, 5417-5421, 1978
A.fritle: Construction and characterization of a 2.5-kilobase procollagen clone.
A.Reference number: I50171; MUID:79074829; PMID:364479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              719 YRADQPS-LRPKDYEVDATLKTLNNQIETLLTPEGSKKNPARTCRDLRLSHPEWSSGFYW 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Match 62.5%; Score 1067; DB 1; Length 964; Local Similarity 60.1%; Pred. No. 4.5e-71; les 185; Conservative 46; Mismatches 63; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               670 NGLPGPIGPAGVRGSHGSQGPAGPPGPPGPPGPPGPPGPPGYEVGF-----
                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                     Accession: I50171
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Best Local S
Matches 185
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A, Note: the compositions of CNBr1, CNBr0, and CNBr2 are identical with those from skin a
A, Note: the compositions of CNBr1, CNBr0, and CNBr2 are identical
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A;Title: Amino acid sequence of cyanogen bromide peptides from the amino-terminal region A;Reference number: A90568; MUID:70131186; PMID:4313735
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A;Reference number: A90557; MUID:69285369; PMID:5809220
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A;Title: Correlation between splicing sites within an intron and their sequence compleme A;Reference number: 150172; MUID:81064671; PMID:6159982
A;Accession: 150172
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A;Cross-references: UNIPARC:UPI00001712DF; EMBL:V00390; NID:g63248; PIDN:CAA23688.1; PID
R;Avvedimento, E.V.; Vogeli, G.; Yamada, Y.; Maizel, J.V.
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A;Molecule type: DNA
A;Residues: 74-92;93,247-431;432,693-774 <WOZ>
A;Cross-references: UNIPARC:UPI00001712Aa; UNIPARC:UPI0000173BB5; UNIPARC:UPI0000173BB6;
R;Fuller, F.; Boedtker, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 'Z',79-95;398-409,'A',411,'V',413-428 <KA2>
A;Cross-references: UNIPARC:UP10000173BB2; UNIPARC:UP10000173BB3
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A;Residues: 'Z',79-95;398-409,'A',411,'V',413-428 <LAN>
A;Cross-references: UNIFARC:UP10000173BB2; UNIPARC:UP10000173BB3
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R; Wozney, J.; Hanahan, D.; Tate, V.; Boedtker, H.; Doty, P.
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A; Title: Structure of the pro alpha-2(I) collagen gene.
A; Reference number: S07327; WUID:82058081; PMID:6272119
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 399-409,'A',411,'V',413-428 <HIG>
A;Cross-references: UNIPARC:UPI0000173BB4
A;Experimental Bource: skin
Biochemistry 8, 2134-2139, 1969
                                                                                                                                                                                                  A,Accession: A90568
A,Molecule type: protein
A,Residues: 'Z',79-92 <KAN>
A,Cross-references: UNIPARC:UP10000173BB1
A,Experimental source: skin
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A;Title: Structural and functional characterization of a splicing mutation in the pro-alf
A;Reference number: 155311; MUID:90368825; PMID:2394758
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A;Molecule type: protein
A;Residues: 23-75,94-96 <WEI2>
A;Cross-references: UNIPARC:UP10000173B98
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                                                                                                              A;Status: translated from GB/EMBL/DDBJ
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A; Molecule type: protein
A; Residues: 32-75, 94-111 <WIR>
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;Molecule type: mRNA
;Residues: 50-126 <CHI>
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N;Alternate names: procollagen alpha 2(1) chain
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence revision 25-Aug-1995 #text_change 31-Dec-2004
C;Acession: A28500; S00824; S09176; I55311; A58111; A28472; A42165; A34405; A90567; I55
A;Molecule type: protein
A;Residues: 121-123,'X',125-134,'X',136-137,'X',139,'XXX',143 <DIX>
A;Residues: 121-123,'X',125-134,'X',136-137,'X',139,'XXX',143 <DIX>
A;Cross-references: UNIPARC:UP10000177397
C;Genetics:
A;Gene: COLIA2
A;Gene: COLIA2
A;Antrone: 36/3; 90/3; 173/1; 236/3; 317/3
C;Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
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                                                                                                                                                                                                                                                                                                                                                                                      62.4%; Score 1066; DB 2; 59.1%; Pred. No. 1.6e-71; iive 47; Mismatches 67
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Best Local Similarity 59.1
Matches 182; Conservative
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A;Molecule type: DNA
A;Readidues: 76-93 «WEIL»
A;Cross-references: UNIPARC:UPI00006F17F; GB:M35391; NID:g189684; PIDN:AAA60041.1; PID:c
A;Accession: A58111
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A;Note: mutant sequence from a partient with Bhlers-Danlos syndrome type VII
A;Note: mutant sequence from a partient with Bhlers-Danlos syndrome type VII
S;Wirtz, M.K.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollister, D.W.
J; Biol. Chem. 262, 16376-16385, 1987
A;Title: Bhlers-Danlos syndrome type VIIB. Deletion of 18 amino acids comprising the N-te
A;Reference number: A28472; MUID:88059013; PMID:3680255
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A;Note: parts of this sequence were determined by protein sequencing; a mutant sequence 1
B;Noti, D: D'Alessio, M: Ramirez, F: Steinmann, B:; Wirtz, M.K.; Glanville, R.W.; Holl
J; Biol. Chem. 264, 16804-16809, 1989
A;Title: Temperature-dependent expression of a collagen splicing defect in the fibroblast
A;Reference number: A34405; WUID:89380311; FWID:2777808
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A;Title: Isolation and characterization of the cyanogen bromide peptides from the alphal A;Reference number: A90567; MUID:71038625; PMID:5529814
A;Reference number: A90567; MUID:71038625; PMID:5529814
A;Reference number: A90567
A;Molecule type: protein
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A;Rosis-references: UNIPARC:UPI0000173890
A;Rosis-references:UPI000017380
A;Rosis-references:UPI0000000
A;Rosis-references:UPI0000
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A,Status: translation not shown; translated from GB/EMBL/DDBJ
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A,Molecule type: DNA, mRNA
A,Molecule type: DNA, mRNA
A,Residues: 145-197 «XUI2>
A,Cross-references: UNIPARC: UPID00016AB4F; GB:M21671; NID:g189521; PIDN:AAAS9994.1; PID:g
A,Cross-references: UNIPARC: UPID00016AB4F; GB:M21671; NID:g189521; PIDN:AAAS9994.1; PID:g
A,Note: single base mutation in intron leads to abnormal splicing of mRNA
R;Chipman, S.D.; Shapiro, J.R.; McKinstry, M.B.; Stover, M.L.; Branson, P.; Rowe, D.W.
J. Bone Minner. Res 7, 733-805, 1992
A,Fitle: Expression of mutant alpha (1)-procollagen in osteoblast and fibroblast cultures A,Reference number: 155485; MUID:92351816; PMID:1642148
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A;Residues: 163-181,200-213 <CH2>
A;Cross-references: UNIPARC:UPI0000071E28; GB:S41099; NID:9252702; PIDN:AAB22761.1; PID:
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
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A;Note: mutant sequence of patient with Ehlers-Danlos syndrome type VIIB
R;Chiodo, A.A.; Hockey, A.; Cole, W.G.
J; Biol. Chem. 267, 6361-6369, 1992
A;Title: A base substitution at the splice acceptor site of intron 5 of the COLIA2 gene
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A;Molecule type: mRNA
A;Residues: 58-108 <WEI3>
A;Cross-references: UNIPARC:UPI0000173B9B; GB:J05049
A;Note: the accession cited by the authors is not found in GenBank
A;Note: parts of this sequence were determined by protein sequencing; a R;Click, E.M.; Bornstein, P.
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PID

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A; Molecule type: mRNA
A; Residues: 964-979, VV, 981-1018, O', 1020 <MYE>
A; Cross-references: UNIPARC:UP10000173BA0; GB:J00114; NID:g180393; PIDN:AAA51996.1; PID::
A; Note: 1019-Leu was also found
R; Wenstrup, R.J.; Cohn, D.H.; Cohen, T.; Byers, P.H.
B ±01. Chem. 253, 7734-7740, 1988
A; Hitle: Arginine for glycine substitution in the triple-helical domain of the products A; Reference number: 155285; MUID:88227975; PMID:2897363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1090-1101,'R',1103-1107 <WEN2>
A;Cross=references: UNIPARC:UPI000016A613; GB:M22817; NID:g179606; PIDN:AAA51846.1; PID:c
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
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C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text change 09-Jul-2004
R;Prockop, D.J.
Submitted to the EMBL Data Library, February 1989
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A;Cross-references: UNIPROT:P02461; UNIPARC:UPI000000CDE; EMBL:X14420; NID:g30057; PIDN
              A;Molecule type: mRNA
A;Residues: 960-1021'L',1023-1188,'D',1190-1197,'S',1199-1356 <MAE>
A;Residues: 960-1021'L',1023-1188,'D',1190-1197,'S',1199-1356 <MAE>
A;Croseriences: UNIPARC:UP1000016A71D; EMBL:X5525; NID:g30101; PIDN:CAA39142.1;
A;Experimental source: fibroblast cell culture
R;Myers, J.C.; Chu, M.L.; Faro, S.H.; Clark, W.J.; Prockop, D.J.; Ramirez, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 3516-3520, 1981
A;Title: Cloning a cDNA for the pro-alpha2 chain of human type I collagen.
A;Reference number: A18855; MUID:81273090; PMID:6267597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1090-1107 <WEN1>
A;Cross-references: UNIPARC:UPI000016A612; GB:M22816; NID:g179602; PIDN:AAA51844.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRYY
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58.1%; Pred. No. 2.5e-67;
tive 46; Mismatches 68
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A;Molecule type: mRNA
A;Residues: 1-1240,'V'
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A;Accession: S09174
A;Molecule type: mRNA
A;Molecule type: mli)
A;Molecule t
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A.Acefesion: A56799
A.Molecule type: mRNA
A.COSS-references: UNIPARC:UPI000016B384; GB:S39878; NID:g1679911; PIDN:AAB19314.1; PID
A.Note: sequence extracted from NCBI backbone (NCBIN:39878, NCBIP:39886)
A.Note: mutant sequence of patient with osteogenesis imperfecta type IV; the authors sugnated sequence.
A.Moleci mutant sequence of patient with osteogenesis imperfecta type IV; the authors sugnated because J.K.; Vuorio, E.
B. Sichim. Biophys. Acta 1049, 171-176, 1990
A.Title: Growth-dependent modulation of type I collagen production and mRNA levels in cu A; Reference number: S10768; MUID:90304220; PMID:2364107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 520-573 <TRO>
A; Residues: 520-573 <TRO>
A; Cross-references: UNIPARC: UPI000073009; GB: M21353; NID: G180881; PIDN: AAA52053.1; PID:
A; Note: single base mutation in intron leads to splicing out of exon 28
B; Bernard, M.P.; Myers, J.C.; Chu, M.L.; Ramirez, F.; Elkenberry, E.F.; Prockop, D.J.
Biochemistry 22, 1139-1145, 1983
A; Title: Structure of a cDNA for the proalpha-2 chain of human type I procollagen. Compa
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                                                              :Title: Comparative study of glycopeptides derived from selected vertebrate collagens. Reference number: A92069; MUID:71001508; PMID:4319110
J. Biol. Chem. 245, 5042-5048, 1970

A,Title: Comparative study of glycopeptides derived from selected vertebrate collagen A,Reference number: A92069; MUID:71001508; PMID:4319110

A,Accession: B92069

A,Molecule type: protein

A,Rederates: UNIPARC: UPI0000140F12

A,Experimental source: skin

A,Note: attachment of 2-0-alpha-D-glucosyl-0-beta-D-galactose to 5-hydroxylysine

A,Note: attachment of 2-0-alpha-D-glucosyl-0-beta-D-galactose to 5-hydroxylysine

R,Fietzek, P. P. Furthmayr, H.; Kuehn, K.

Bur. J. Biochem. 47, 257-261, 1974

A,Title: Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-1

A,Reference number: A91224; MUID:75008198; PMID:4412529

A,Accession: A91224

A,References: 1418-447 eFIE>

A,References: 1418-447 eFIE>

A,References: 1418-447 eFIE>

A,Cooss-references: UNIPARC: UPI0000173B9E

A,Title: Single base mutation in the pro alpha 2(1) collagen gene that causes efficies

A,Reference number: 159125; MUID:88276936; PMID:2839839
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A;Molecule type: mRNA
A;Residues: 663-675,'V',677,'P',679-742,'A',744-746 <FOR>
A;Residues: 663-675,'V',677,'P',679-742,'A',744-746 <FOR>
A;Residues: 663-675,'V',677,'P', 679-742,'A',744-746 <FOR>
A;References: UNIPARC: UDIO00006E0A7; GB: L47668; NID:g1009095; PIDN:AAB59577.1;
B;Niythizi, C.; Bonadio, J.; Byers, P.H.; Byre, D.R.
J. Biol. Chem. 267, 23108-23112, 1992
A;Title: Incorporation of type I collagen molecules that contain a mutant alpha 2(I)
A;Reference number: I55369; MUID:93054637; FMID:1385413
A;Status: translated from GB/EMBL/DDBJ
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A; Molecule type: mRNA
A; Residues: 665-666, 'D', 668-670 <NIY>
A; Cross-references: UNIPARC:UP1000011E7D9; GB:L00613; NID:g180888; PIDN:AAB59384.1;
A; Note: mutant sequence from a patient with osteogenesis imperfecta
B; Bateman, J.F.; Hannagan, M.; Chan, D.; Cole, W.G.
Biochem. J. 276, 765-770, 1991
A; Title: Characterization of a type I collagen alpha 2(I) glycine-586 to valine subs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: I59125
A,Status: translation not shown; translated from GB/EMBL/DDBJ
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PID:

63

Gaps

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Biochemistry 17, 3404-3411, 1978
A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr per
A;Reference number: A90414; MUID:79000343; PMID:687591
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Rjide, B.; Vitale, B.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
V. Biol. Chem. 266, 5256-5259, 1991
Ajütle: G to T transversion at position +5 of a splice donor site causes skipping of the
AjReference number: 155349; MUID:91161621; PMID:1672129
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;Residues: 537-605 <LEE>
;Cross-references: UNIPARC:UPI0000004A2; GB:M59312; NID:g180815; PIDN:AAA52041.1; PID:<
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A;Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping and A;Reference number: A38303; MUID:91009133; PMID:2145268
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A;Residues: 861-1015 <COL>
A;Cross-references: UNIPARC:UP100000004A1; GB:J05617; GB:M55603; GB:M59227; NID:9180878;
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos sync
R;Mankoo, B.S.; Dalgleish, R.
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A; Mesidues: 96-979, A', 981-984, PS', 987, QN', 990-1096, P', 1098-1152, AT', 1155, S', 1157-1
A; Residues: 96-979, A', 981-984, PS', 987, QN', 990-1096, P', 1098-1152, AT', 1155, S', 1157-1
A; Cross-references: UNIPARC: UD10000173B87
A; Experimental source: liver
R; Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myer
R; Loidl, H.R.; Brinker, J. 938-939, Myer
A; Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollager
A; Reference number: A93551; MUID: 85087944; PMID: 6096827
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A; Residues: 1065-1155, °P., 1157-1466 <LOI>
A; Cross-references: UNIPARC:UD10000173B88; EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAJ
A; Cross-references: UNIPARC:UD10000173B88; EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAJ
R; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantl
Biochemistry 25, 1408-1413, 1986
A; Title: Human type III collagen gene expression is coordinately modulated with the type
A; Reference number: I52393; MUID:86187804; PMID:3754462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
A;Cross-references: UNIPARC:UPI000016A6B5; GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A.Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CBS from tyr A;Reference number: A90438; MUID:80198282; PMID:6246925
A;Accession: A90438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end.
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A;Title: Human pro alphal(III) collagen: cDNA sequence f
A;Reference number: S02119; MUID:88189827; PMID:3357782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 728-895,'A',897-964 <SEY4>
A;Cross-references: UNIPARC:UP10000173B85
                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 399-675,'N',677-727 <SEY3>
A;Cross-references: UNIPARC:UP10000173B84
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A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                       A; Accession: A90414
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A;Reference number: IS1868
A;Accession: IS1868
A;Accession: IS1868
A;Accession: IS1868
A;Accession: Prelimary; translated from GB/EMBL/DDBJ
A;Accession: Prelimary; translated from GB/EMBL/DDBJ
A;Accession: B6-194 AMIL>
A;Residues: 186-194 AMIL>
A;Across-references: UNIPARC:UPIO000000B14; GB:S62925; NID:9386425; PIDN:AAD13937.1; PID: B;Chem. J. 311, 939-943, 1995
Biochem. J. 311, 939-943, 1995
Biochem. J. 311, 939-943, 1995
A;Fitle: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3 A;Reference number: S59511; MUID:96067614; PMID:7487954
A;Accession: S59511
A;Accession: S59511
A;Accession: S69512
A;Accession: S69513
A;Accession: S69513
A;Accession: S69513
A;Accession: S69514
A;Accession: S69515
A;Cross-references: UNIPARC:UPI0000173B83; GB:S79877; NID:91195576; PIDN:AAB35615.1; PID
                                                                                                                                                                                                                                                                                                    A;Accession: S04642
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1-1196 <ALA>
A;Cross-references: UNIPARC:UPI0000173B80; EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID
A;Note: the complete sequence is not shown
A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene (A;Reference number: PE0011; MUD:89378752; PMID:2777083
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A; Residues: 149-163, 'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,
A; Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,
A; Cross = references: UNIPARC:UP1000016A61C; EMBL:X15332; NID:929545; PIDN:CAA33387.1; PID
A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
B; Seyer, J.M.; Kang, A.H.
Biochemistry 16, 1158-1164, 1977
A; Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A; Reference number: A90399; MUID:77134724; PMID:557335
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A;Residues: 'V'.169-225, 229-232,'P',234-292,'D',294-398 <SEY1>
A;Residues: 'V'.169-225, 229-232,'P',234-292,'D',294-398 <SEY1>
A;Cross-references: UNIPARC:UP10000173B81
A;Experimental source: liver
A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R;Seyer, J.M.
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A; Residues: 1-170 < TON
A; Residues: 1-170 < TON
A; Residues: 1-170 < TON
A; Cross=references: UNIPARC: UPI000016A706; EMBL: X07240; NID: 930060; PIDN: CAA30229.1; PID
A; Cross=references: UNIPARC: UPI000016A706; EMBL: X07240; NID: 930060; PIDN: CAA30229.1; PID
B; Janeczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A; Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A; Reference number: S04887; MUD: 89386015; PMID: 2780304
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A; Residues: 1-176 <BEN>
A; Cross-references: UNIPARC: UP1000016A703; GB: M26939; NID: g180813; PIDN: AAA52040.1; PID: A; Cross-references: UNIPARC: UP1000016A703; GB: M. G. Crombrugghe, B. Nucleic Acids Res. 16, 7201, 1988
A; Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre A; Reference number: S01726; MUID: 88303360; PMID: 3405773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 'V', 169-225, 229-277,'A', 279-292,'D',294,'S',296-398 <SEY2>
A; Residues: 'V', 169-225, 229-277,'A', 279-292,'D',294,'S',296-398 <SEY2>
A; Cross-references: UNIPARC: UP10000173B82
A; Experimental source: liver
A; Note: author submitted corrections to A90399
R; Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. Genet. 53, 62-70, 1993
A; Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A;Title: Structure of cDNA clones coding for the entire prepro-alphal(III) chain of
                                                                                                                                                                                        erences.
A,Reference number: S04642; MUID:89350838; PMID:2764886
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Search completed: April 26, 2006, 16:20:16 Job time : 29.4247 secs

1450 GGPDQEFGVDVGPVCFL 1466

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Filos-1093/Region: cell attachment (R-G-D) motif
Filos-1093/Region: cell attachment (R-G-D) motif
Filos-1221/Region: carboxyl-terminal nonhelical telopeptide
Filos-1221/Region: carboxyl-terminal propeptide #status predicted <CPR>
Filos-1466/Domain: carboxyl-terminal propeptide defected corpoxyl-terminal homology <FCC>
Filos-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
Filos-14/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
Filos-14/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
Filos-1212/Modified site: allysine (Lys) #status predicted
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arπ
A;Reference number: I59025; MUID:85216505; PMID:3858826
                            A; Reference number: 159025; MID:85216505; PMID:3858826
A; Accession: 179359
A; Residues: 1165-1196 «EWA>
A; Robert (Ewa)
A; Robert (Ewa)
A; Reference number: A92516; MuID:85157600; PMID:2579949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: structural component of extracellular fibrous polymer that maintains inte C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Reywords: coilade coil; Bhlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd F; 1-23/Domain: signal sequence #status predicted <SIG>F; 24-153/Domain: amino-terminal propeptide #status predicted <PRO>F; 31-31/Domain: von Willebrand factor type C repeat homology <VWC>F; 154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>F; 154-167/Region: amino-terminal nonhelical telopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 2q31-2q31
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dar C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide ter of their length, is formed with desmosine cross-links made from lysine and allysine a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: UNIPARC:UP10000173B89; GB:M10615; GB:M10793; GB:M10794; GB:M10795; A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Comment: Prolines and lysines at the third position of the tripeptide repeating unit 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1153 TSGHPGPIGPPGPRGRRGSRGSPGHPGQPGPPGPPGAPGPCCGGVGAAAIAGIGGEK 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 WKSGEYWIDPNQCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMTDGFQFEYGGQGSDPADVA-IQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 LLLKGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGA-----GFDFSFLPQPPQEK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:118729; OMIM:120180
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Best Local Similarity 60.33
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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A Ala-Kokko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
A Ala-Kokko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
A Ala-Kokko L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFO11718; AAB94064.2; -; Genomic_DNA.
BROS GO:0005581; C:collagen; IEA.
R GO; GO:0005581; C:cotlagen; IEA.
R GO; GO:0005501; F:extracellular matrix structural constituent; IEA.
R GO; GO:000581; P:extracellular matrix structural constituent; IEA.
R GO; GO:000581; P:phosphate transport; IEA.
R InterPro; IPR0008161; CIG helix.
R InterPro; IPR0008161; CIG helix.
R InterPro; IPR0008161; I.B.
R Fram; PF01440; COLFI; 1.
R ProDom; PD0020707; CIG helix; 3.
R ProDom; PD002077; CIG helix; 3.
R ProDom; PD002078; Fib_collagen_C; 1.
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                                                               Prockop D.J.;
"Analysis of the COLIA1 and COLIA2 genes by PCR amplification and scanning by conformation-sensitive gel electrophoresis identifies (COLIA1 mutations in 15 patients with osteogenesis imperfecta type identification of common sequences of null-allele mutations.";
Am. J. Hum. Genet. 62:98-110(1998).
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Q9UMM7;
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                          WEDLINE=98107942; PubMed=9443882;
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MEDLINES-89025644; PUMPde=3178743;
Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockup D.J.;
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of human type I procollagen:";
Biochem. J. 253:919-922(1998).
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MEDLINE=85190558; PubMed=3857621;

Barsh G.S., Roush C.L., Bonadio J., Byers P.H., Gelinas R.E.;

"Intron-mediated recombination may cause a deletion in an alpha 1 type I collagen chain in a lethal form of osteogenesis imperfecta.";

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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Click B.M., Bornstein P.; "Isome cyanogen bromide peptides from "Isolation and characterization of the cyanogen bromide peptides from the alpha 1 and alpha 2 chains of human skin collagen."; Biochemistry 9:4699-4706(1970).
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MEDLINE-93352646; PubMed=8349697;
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"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I)
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MEDLINE-88329734; PubMed=2843432; DOI=10.1016/0378-1119(88)90013-3;
                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of the region encompassing the first twenty-five exons of the human pro alpha 1(1) collagen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1-181.
MEDLINE=84270697; PubMed=6462220;
Chu M.-L., de Wer W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez F.;
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conservation of a pattern of introns and exons.";
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Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
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Pred. No. 1.8e-116;
1; Mismatches 0; Indels 0;
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R. Manner D.M., Rayminski M.I., Shalska U., Shal
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                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 7.6e-115;
2; Mismatches 2; Indels 0;
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R Submitted (AUG-2012) to the EWBL/GenBank/DDBJ databases.

EMBL; BC036531; AAH36531.1; -; mRNA.

GO; GO:0005581; C:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituer

GO; GO:0005201; F:extracellular matrix structural

R GO; GO:0005201; F:extracellular matrix

EnterPro; IPR008161; C:gybelix.

R InterPro; IPR008161; C:gybelix.

R InterPro; IPR001805; Fib_collagen.

R InterPro; IPR001805; VWF_C.

R Ffam; PF01410; CCLFT; 1.

R Pfam; PF01410; CCLFT; 1.

R ProDom; PD000007; Cig helix; 3.

R ProDom; PD000007; Cig helix; 3.

R SWART; SM00038; Fib_collagen_C; 1.

SWART; SM00034; VWC; 1.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local Similarity 98.7°
Matches 305, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDPNQCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEYGGOGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 242
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Ohara O., Nagage T., Kikuno F.R.;
"None Title.";
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Last annotation update)
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Last annotation update)
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Pred. No. 3.5e-116;
2; Mismatches 0;
                                                                                                                                                                          PRT; 1467 AA
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                                                                                                                                                                                                                                                                                                                                                 Collagen alpha 1 chain variant (Fragment).
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01-0CT-2002 (TrEMBLrel. 22, Last sequen
01-MAR-2004 (TrEMBLrel. 26, Last annota
Alpha 1 type I collagen, preproprotein.
                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                          Q59F64 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8N473 HUMAN PRELIMINARY;
Q8N473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 307; Conservative
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1456 FDVGPVCFL 1464
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custatation-the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE-2103337; PubMed=11147834; DOI=10.1006/abbi.2000.2099;
Campbell B.G., Wootton J.A.M., MacLeod J.N., Minor R.R.;
Sequence of normal canine CCLIA1 cDNA and identification of a heterozygous alphal(I) collagen Gly208Ala mutation in a severe case of canine osteogenesis imperfecta.";
Arch. Biochem. Biophys. 384:37-46(2000).
I- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
I- SUBUNIT: Triners of one alpha 2(I) and two alpha 1(I) chains.
I- FTW. Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
I- DYR. Prolines at the collagen of a cause of osteogenesis imperfecta
                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF153062; AAD34619.1; -; mRNA.

R Ensembl; ENSCAFC0000017018; Canis familiaris.

R InterPro; IPR00161; C1g_helix.

R InterPro; IPR001616; Collagen.

R InterPro; IPR001607; VWF_C.

R InterPro; IPR001007; VWF_C.

R Pfam; PF01410; Collagen; 18.

R ProDom; PD002078; Fib_collagen_C; 1.

R ProDom; PD02078; Fib_collagen_C; 1.

R PROSITE; PS01208; VWFC_1; 1.

R ROSITE; PS01208; VWFC_2; 1.

R Collagen; Disease mutaFion; Extracellular matrix; Glycoprotein; W Hydroxylation; Pyrrolidone carboxylic acid; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allysine (By similarity).
5-hydroxylysine (By similarity).
3-hydroxyproline (By similarity).
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Triple-helical region.
Nonhelical region (C-terminal).
Cell attachment site (Potential)
Cell attachment site (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
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N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE, AND VARIANT OI ALA-208
                                                                                                                                                                                                                                                                                                                 Collagen alpha 1(I) chain precursor Name=COLIA1;
                                                                                                                                                                                   PRT;
                                                                                                                                                                                   STANDARD;
1456 FDVGHVCFL 1464
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                                                                                                                                                                       63 YRADDANVVRDRDLEVDITLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
                                                                                                                                                                                                                                                                                        123 IDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ
                                                                                                                                                                                                                                                                                                                                                         183 FEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE
                                                                                                                                                                                                                                                                                                                                                                                                                            243 IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIBYKTTKSSRLPIIDVAPLDVGAPDQEFG
                                                                                                                                                     3 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88056316; PubMed=3678834; DOI=10.1016/0378-1119(87)90159-4; Finer M.H., Boedtker H., Doty P.; "Construction and characterization of cDNA clones encoding the 5' end of the chicken pro alpha 1(I) collagen mRNA."; Gene 56:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.,
Gross J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Anino acid sequence of chick skin collagen alpha 1(I)-CBB and the complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE OF 1-144.

MEDLINE=88007542; PubMed=2820966;

Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;

Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;

"Unusual DNA sequences located within the promoter region and the first intron of the chicken pro-alpha 1(1) collagen gene.";
O-linked (Gal. . .) (By similarity)
N-linked (GlcNAc. . .) (By similarighty)
A (In Ol; severe).
WW, 58E3674D2B570697 CRC64;
                                                                                                                    ;
                                                                                  DB 1; Length 1460;
                                                                                                                    4; Indels
                                                                                 97.5%; Score 1664; DB 1;
97.1%; Pred. No. 3.5e-114;
ive 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1453 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 21:2048-2055(1982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 1-153.
                                                   138762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 152-1187
                                                                                                                  Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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208
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261 26
1361 136
208 20
1460 AA;
                                                                                                  Similarity
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CARBOHYD
                                 VARIANT
SEQUENCE
                                                                                  Query Match
                                                                                                      Local
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                       Eyre D.R., Glimcher M.J.;
"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                                                                                                                                                        NUCLECTIDE SEQUENCE OF 1311-1453.
MEDLINE-80134546; PubMed-6987088; DOI-10.1016/0014-5793(80)80761-7;
                                                                                                                                                                                                                                                                                                                                                                   Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T., Pastan I., Decrombrugghe B., Fietzek P.P., Olsen B.R.;
"Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(1)-chains.";
FEBS Lett. 11:61-65(1980).
-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
-!- SUBUNT Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICTY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                   NUCLEOTIDE SEQUENCE OF 981-1453.
MEDLINESH160715. PubMed=6927845;
MLDLINESH160715. PubMed=6927845;
Fuller F., Boedtker H.;
"Sequence determination and analysis of the 3' region of chicken px "Sequence determination and analysis of the 3' region of chicken px alpha 1(1) and pxro-alpha 2(1) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences.";
Biochemistry 20:996-1006(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxyapatite.
PTM: Proline residues at the third position of the tripoptide PTM: Proline residues at the third position of the tripoptide chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X.
SIMILARITY: Belongs to the fibrillar collagen family.
SIMILARITY: Concains 1 VWPC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO1208; VWFC_1; 1.

PROSITE; PSSO184; VWFC_2; 1.

COllagen; Direct protein sequencing; Extracellular matrix;

Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat;

Signal; Structural protein.

Signal | N-terminal propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrrolidone carboxylic acid.
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Collagen alpha 1(I) chain.
C-terminal propeptide.
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EMBL; W17838; AAA48704.1; O'DINED; Genomic_DNA.

EMBL; VOO401; CAA23695.1; -; MRNA.

EMBL; M10571; AAA48671.1; ALT_SEQ; MRNA.

EMBL; M17607; AAA48672.1; -; MRNA.

PIR; A27179; A27149.

PIR; 150629; 150629.
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InterPro; IPR00816; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR001007; VWF_C.
Pfam; PP01391; Collagen; 18.
Pfam; PP01391; Collagen; 18.
Pfam; PP00309; VWC; 1.
ProDom; PD000007; Clg_helix; 2.
SYART; SW00038; COLFI; 1.
SWART; SW00214; VWC; 1.
  WEDLINE=72243016; PubMed=5047697;
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In J. Dent. Res. 78:11-1919.

REAL, 278279; CARBOIG33.1; -; mRNA.

EMBL, 278279; CARBOIG33.1; -; mRNA.

EMBL, 278279; Caycoplasm; IEA.

RO; GO:0005581; C:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005215; F:protein binding; IEA.

GO; GO:0007155; P:collagen; IEA.

RO; GO:0006817; P:phosphate transport; IEA.

RO; GO:0006817; P:phosphate transport; IEA.

RITHERPO; IPR0008160; Collagen.

RITHERPO; IPR001007; VWF_C.

PÉRM; PF01410; COLFI; 1.

REPTO; PF01410; COLFI; 1.

REPTO; REPTO; PF000007; C19_helix; 3.
                                                                                                                                                                                                                                                                                                                                                                                                    63 YRADDANVYRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                    Gaps
                  1153 3-hydroxyproline.
254 O-linked (Gal. ..) (By similarity).
1354 N-linked (GloNAc. ..) (By similarity).
1187 F -> L (in Ref. 5).
1441 Q -> H (in Ref. 6).
AA; 137789 MW; 3BC6152134271F4D CRC64;
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                                                                                                                                                                                                   Length 1453;
5-hydroxylysine (Potential).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collagen alphal (Fragment).
                                                                                                                                                                                                93.2%; Score 1591; DB 1;
90.3%; Pred. No. 8.8e-109;
live 21; Mismatches 9;
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                                                                                                                                                                                                                  Local Similarity 90.3
Les 279; Conservative
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Q63079 RAT PRELIMINARY;
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1445 IDIGPVCFL 1453
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303 FDVGPVCFL 311
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581 LDIGPACFV 589
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NCBI_TaxID=10090;
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Name=Collal;
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NUCLEOTIDE
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X. MEDLINE=22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

A. Klauener R.D., Colline F.A., Grouse L.H., Derge J.G.,

A. Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A. Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

B. Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

B. Rownstein M.J., McKernan K.J., Malek J.A., Gunzatne P.H.,

R. Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

M. Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                    3 NGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPGPPGAPGFDFSFLPQPPQEKAHDGGRY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                   Length 1453;
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1453 AA; 137886 MW; E6896BDC19A4A1D8 CRC64;
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Last annotation update)
                                                                                                                Query Match 93.2%; Score 1591; DB 2; Best Local Similarity 90.9%; Pred. No. 8.8e-109; Matches 281; Conservative 16; Mismatches 12;
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ProDom; PD002078; Fib_collagen_C; SMART; SM00038; COLFI; 1. SMART; SM00214; VWC; 1.
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(991L6)
(091L6)
(01-UN-2001 (TEMBLE1. 17, C1
01-UN-2001 (TEMBLE1. 17, L6
01-MAR-2004 (TEMBLE1. 26, L6
COllal protein (Fragment).
Name=Collal;
Mus musculus (Mouse).
                                        PROSITE; PS01208; VWFC_1; 1. PROSITE; PS50184; VWFC_2; 1.
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NCBI_TaxID=10090;
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                                                                Collagen.
NON TER
SEQUENCE
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281 NGLPGPIGPPGPRGRIGDSGPAGPPGPPGPPGPPSGGYDFSFLPQPPGEKSQDGGRY 340
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                          month old
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A strausberg R.;
MGI: 88467; Collai. -; mRNA.
MGI: 88467; Collai. -; mRNA.
R GO; GO: 6005615; C: extracellular space; TAS.
R InterPro; IPR008161; Collagen.
R InterPro; IPR008160; Collagen.
R InterPro; IPR00885; Fib_collagen_C.
Fram; PF01410; CoLr; 1.
R ProDom; PD000007; Clg_helix; 1.
R ProDom; PD000007; Clg_helix; 1.
R ProDom; PD002078; Fib_collagen_C; 1.
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Last annotation update)
                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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90.9%; Pred. No. 4.8e-109;
iive 15; Mismatches 13;
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QEPCL3;
05-JUL-2004 (TEMBLEE). 27,
05-JUL-2004 (TEMBLEE). 27,
05-JUL-2004 (TEMBLEE). 27,
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Matches 281; Conservative
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STRAIN=Mix FVB/N;
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90.9%; Pred. No. 1.2e-108;
ive 15; Mismatches 13; Indels
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TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
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  TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059281; AAH55281.1; -; mRNA.
MGI; MG1:88467; Collal.; -; mRNA.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR008161; Clg helix.
InterPro; IPR00885; Fib collagen.
InterPro; IPR00885; Fib collagen.
InterPro; IPR00885; Fib collagen.
InterPro; IPR001007; VWF.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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ProDom; PD000007; Clg_helix; 2.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; CCLFI; 1.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1074; Man N.K.,

MEDLINE=2288257; Medline F.S., Medline G.M., Medline G.M., Medline C.M., Medline C.
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
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                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
10-MX-2005 (TrEMBLrel. 30, Last annotation update)
10-MX-2013 type I, alpha 1.
Name=Colla1; ORFNames=RP23-112C19.9-001;
Mus musculus (Mouse).
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EMBL; ALG65480; CA123970.1; -; Genomic_DNA.
EMBL; ALG62790; CA123970.1; -; Genomic_DNA.
EMBL; ALG62790; CA123970.1; JOINED; Genomic_DNA.
EMBL; ALG66480; CA12380.1; JOINED; Genomic_DNA.
EMBL, BNSWUSG000001506; Mus musculus.
MGI; MGI:88467; Colla1.
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR001005; WF.C.
InterPro; IPR001007; WF.C.
Pfam; PF01410; CoLF1; 1.
Pfam; PF01410; CoLF1; 1.
Pfam; PF01491; Collagen; 18.
     PRT; 1453 AA
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Probom; PD0000708; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
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Q810J9 MOUSE PRELIMINARY;
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NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                       YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW 122
                                                                                                                                                                                                                                                                                                                                                         IDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 182
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Biochim. Biophys. Acta 1216:469-474(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse pro alpha 1(I) chain
of type I procollagen.";
Matrix Biol. 14:593-595(1995).
                                                                                                                                                                                       3 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY
                                                                                                                                              Gaps
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MEDLINE=94092741; Pubmed=8268229; DOI=10.1016/0167-4781(93)90016-7;
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                                                                                                   Length 1453;
                                                                                                                                              13; Indels
                                                            1453 AA; 138032 MW; 0B7F06BBB9A1D5EA CRC64;
                                                                                                   93.0%; Score 1588; DB 2;
90.9%; Pred. No. 1.5e-108;
ive 15; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOIAI MOUSE STANDARD; PRT; 1453 AA. P11087; Q53WT0; Q66053; Q61367; Q61427; Q63919; O1-JUL-1989 (Rel. 11, Created). O1-WOV-1997 (Rel. 35, Last sequence update). 13-SEP-2005 (Rel. 48, Last annotation update). Collagen alpha II. Chain precursor. Name-Collal; Synonyms-Collal; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an indirect mechanism.";
Mol. Cell. Biol. 14:5950-5960(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6; TISSUE=Liver;
MEDLINE=94344105; PubMed=8065328;
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MEDLINE=96033240; PubMed=8535610;
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PROSITE; PS01208; VWFC_1; 1. PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                            Conservative
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1445 LDIGPACFV 1453
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281; Conserv
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                                                                SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mooslehner K., Harbers K.;
"Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size of
                                French B.T., Lee W.-H., Maul G.G.; "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-I- SIMILARITY: Belongs to the fibrillar collagen family.
-I- SIMILARITY: Contains 1 WWFC domain.
-I- CAUTION: Ref. 3 sequence differs from that shown due to erroneous gene model prediction.
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MEDLINE=84170331; PubMed=6324198;
Harbers K., Kuehn M., Delius H., Jaenisch R.;
"Insertion of retrovirus into the first intron of alphal(I) collagen gene leads to embryonic lethal mutation in mice.";
Proc. Natl. Acad. Sci. U.S.A. 81:1504-1508(1984);
                                                                                                                                                                                                                                           Monson J.M., Friedman J., McCarthy B.J.;
"DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene:
"Sydence for a mouse Bl element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
MEDLINE=86137403; PubMed=3841523; DOI=10.1016/0378-1119(85)90329-4;
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 735-878 AND 1005-1058.
MEDLINE=83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
Midentification of a Balb/c mouse pro alpha 1(I) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
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Blochim. Blophys. Acta 1089:241-243(1991).
-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- SUBUNIT: Froms the fibrils of tendon, ligaments an bones. In bones the fibrils are mineralized with calcium
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Metsaeranta M., Toman D., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse type I, II, III and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAA37333.1; -; mRNA.
| AAA37334.1; -; Genomic_DNA.
| AAA37332.1; -; Genomic_DNA.
| AAA37332.1; JOINED; Genomic_DNA.
| AAA37332.1; JOINED; Genomic_DNA.
| AAA37332.1; JOINED; Genomic_DNA.
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S67530; AAB29424.1; -; Genomic DNA.
S67482; -; NOT ANNOTATED CDS; Genomic DNA
X54876; CAA38657.1; ALT SEQ; Genomic DNA.
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Nucleic Acids Res. 16:773-773(1988)
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                                                                                                                       Gene 39:311-312(1985)
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63 YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW 122
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; U03419; AAA03475-1; -; mRNA.
MG1; MG1:88467; Colla1.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 1.
ProDom; PD002078; Fib_collagen_C; 1.
SNART; SM00038; COLFI; 1.
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90.4%; Score 1543; DB 2; Length 3
Best Local Similarity 88.7%; Pred. No. 4.9e-106;
Matches 274; Conservative 15; Mismatches 20; Indels
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325 AA; 35229 MW; A5A21B74DFDE3EF1 CRC64;
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Last annotation update)
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
Alpha-1 type I procollagen (Fragment)
Name=Collal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. 
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R EMBL; K01688; AAA37330.1; -; Genomic_DNA.
R EMBL; X16596; CAA39927.1; -; Genomic_DNA.
R EMBL; X16596; CAA33904.1; -; Genomic_DNA.
R EMBL; X15981; CAA41046.1; -; Genomic_DNA.
R PIR; S57243; S21626.
R Ensembl; ENSWUGS00000001506; Mus musculus.
R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR008161; C1g helix.
InterPro; IPR008161; C1g helix.
InterPro; IPR008160; Collagen.
R InterPro; IPR001007; VWF_C.
P Fam; PF011391; Collagen.
R Probom; PD000007; C1g_helix; 3.
R Probom; PD000007; C1g_helix; 3.
R Probom; PD000077; C1g_helix; 3.
R PROSTITE; SM00214; VWC; 1.
R SMART; SM00014; VWC; 1.
R PROSTITE; PS501084; VWRC 1; 1.
R PROSTITE; SM002178; ARGEDILIAR matrix; Glycoprotein; Hydroxylation; PTX111 matrix; Glycoprotein; Hydroxylation; My Pytrolidone carboxylic acid; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WWFC.
Nonhelical region (N-terminal).
Triple-helical region (C-terminal).
Nonhelical region (C-terminal).
Cell attachment site (Potential).
Cell attachment site (Potential).
Pyrrolidone carboxylic acid (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
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Matches 277, Conservative
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InterPro; IPR008160; Collagen.
InterPro; IPR00885; Flb_collagen_C.
Pfam, PF01410; COLFF; 1.
SMART; SM00038; COLFI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q640B2 XENTR PRELIMINARY;
                                                                                                                                                                                                                                                   Best Local Similarity 96.5
Matches 277; Conservative
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                                               NUCLEOTIDE SEQUENCE
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 302
                                                            IDPNOGCNLDAIKVPCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE
                                                                                                                                                                                                                                                                                                                                                                  NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY
        Cynops pyrrhogaster (Japanese common newt).
Bukaryota; Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
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0
                                                                                                                                                                                                                                                                                                                            Length 1450;
                                                                                                                                                                                                                                                                                                                                                18; Indels
                                                                                                                                                                                                                                                                                                         1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                           89.9%; Score 1534; DB 2;
86.7%; Pred. No. 1.5e-104;
cive 23; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 AA
                                                                                                                                                                                                                                                                             PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDB_BOVIN
Q95NDB_BOVIN PRELIMINARY;
Q95NDB;
01-DEC-2001 (TEMBLEEL: 19, Lo
01-DEC-2003 (TEMBLEEL: 19, Lo
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.7
Matches 268; Conservative
Alpha 1 type I collagen.
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IDIGPVCFL 1450
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                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                Collagen.
SEQUENCE
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LSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDDNQCCNLDAIKVFCNMETGE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCVYPTQPSVAQKNWYISKNPKEKRHVWYGESMTGGFQFEYGGGGSDPADVAIQLTFLRL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 LSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMETGE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYGGGGSDPADVAIQLTFLRL 204
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                               Grosse-Hovest L., Brem G.;
Submitted (MAY-2001) to the BMBL/GenBank/DDBJ databases.
BMBL; AJ312110; CAC38832.1; -; Genomic_DNA.
BMBL; AJ312110; CAC38832.1; JOINED; Genomic_DNA.
BMBL; AJ312111; CAC38832.1; JOINED; Genomic_DNA.
BMBL; AJ312112; CAC38832.1; JOINED; Genomic_DNA.
GQ; GG:0005581; C:collagen; IEA.
GQ; GG:0005737; C:cytoplasm; IEA.
GQ; GG:0005201; F:extracellular matrix structural constituent; IEA.
GQ; GG:000617; P:phosphate transport; IEA.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lauraaiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xengus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVGPVCFL 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
287 AA; 31698 MW; A9122CAEB7DC3DAE CRC64;
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Last annotation update)
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Yilalon D.K., Muzny D.M., Sodesgren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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TISSUE-Whole body;

A Tain S. , Gerhard D.S.;

Klein S. , Gerhard D.S.;

Kabbit BO0820118; AAH82718.1; -; mRNA.

EMBL; BEO820118; AAH82718.1; -; mRNA.

EMBL; BC0820118; Flextracellular matrix structural constituent; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005017; Flextracellular matrix structural constituent; IEA.

RO; GO:0006117; Flextrace
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85.8%; Pred. No. 1.6e-102;
ive 25; Mismatches 18; Indels
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PROSITE; PS50184; VWFC_2; 1.
Collagen; Hypothetical_protein.
SEQUENCE 1499 AA; 137539 WW; 45663981687A3B4B CRC64;
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Best Local Similarity 85.8°
Matches 266; Conservative
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Sequence 19,
Sequence 19,
Sequence 19,
Sequence 19,
Sequence 4, P
Sequence 5, P
Sequence 5, P
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1707
1 RSNGLPGPIGPPGFRGRTGD......LDVGAPDQEFGFDVGFVCFL 311
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-289-578-9
US-09-289-578-9
US-08-9531-347C-21
US-08-953-825-18
US-09-570-811-18
US-09-570-811-18
US-09-588-608-18
US-09-588-608-18
US-09-570-811-20
US-09-570-811-20
US-09-570-811-20
US-09-570-811-10
US-09-588-882-10
US-09-589-578-10
US-09-589-578-10
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US-09-589-578-10
US-09-589-581-19
US-09-589-881-19
US-09-589-3881-19
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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No.
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8 639 37.4 1806 2 US-09-919-497-56 Sequence 56, Appl 543.5 31.8 1745 2 US-09-949-0024405 Sequence 40. Appli 6 543.5 31.8 1745 2 US-09-949-0024405 Sequence 40. Appli 2 Sequence 40. Appli 2 Sequence 30. Appli 2 US-09-949-002492 Sequence 2, Appli 3 394.5 23.1 1107 2 US-09-795-061-2 Sequence 2, Appli 3 394.5 23.1 1107 2 US-10-153-469A-11 Sequence 11, Appli 6 392 23.0 1388 2 US-10-163-469A-10 Sequence 11, Appli 8 2 US-10-104-889-10 Sequence 10, Appli 9 375 22.0 1169 2 US-10-104-044-89-10 Sequence 6, Appli 1 375 22.0 1169 2 US-10-104-049-6 Sequence 6, Appli 1 375 22.0 1169 2 US-10-104-889-6 Sequence 6, Appli 1 375 22.0 1169 2 US-10-104-889-8 Sequence 8, Appli 3 372 21.8 219 2 US-10-1153-469A-6 Sequence 8, Appli 3 372 21.8 219 2 US-10-1153-469A-6 Sequence 6, Appli 3 372 21.8 219 2 US-10-1153-469A-6 Sequence 6, Appli 3 372 21.8 219 2 US-10-1153-469A-6 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Sequence 44, Appli 3 372 21.8 219 2 US-10-1164-889-44 Se	ALIGNMENTS		Query Match 99.3%; Score 1695; DB 2; Length 1461; Best Local Similarity 99.7%; Pred. No. 1.6e-141; Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps	3 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGPDFSFLPQPPQEKAHDGGRY	3 8	1213 YRADDANVVRDRDLEVDTTLKSLGQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW	123 IDPNGCNLDAIKVPCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ	12/3 IDPNÇGCNLDAIKVFCNMEIGEICVYFIQESVAQKNWIISKNFKDKKHVWFGESMIIDGFQ 183 SEVZGQGGDBADVAIGITEIBIMGTERSCONITTVHCKNSVAVMDONGNIKKAIIIKKGNR	1333 FEYGGGGSDPADVALULI EMERS IERSQNI I INCONSVATIDO V INCONSTRUCTORIA INCONST
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APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1396 IEIRAEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKTSRLPIIDVAPLDVGAPDQEFG 1455
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                        Score 1695; DB 2;
Pred. No. 1.6e-141;
1; Mismatches 0;
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FILING DATE:
FILING BATE:
APPLICATION: 436
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08963825; Patent No. 6110689; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible ODERATING SYSTEM: PC-DOS/MS-
1999-08-17
                    NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1464
                                                                                                                                                                                          Query Match
Best Local Similarity 99.7%;
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1456 FDVGPVCFL 1464
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 FDVGPVCFL 311
                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
  CURRENT FILING DATE:
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US-08-963-825-18
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APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Me
TITLE OF INVENTION: obtaining Such and Their Uses
FILE REPERENCE: 1149-3
CURRENT APPLICATION NUMBER: US/09/331,347C
                                                                                                                                                                        Sequence 9, Application US/09289578;
Sequence 9, Application US/09289578;
Sequence 9, Application US/09289578;
GENERAL INFORMATION:
APPLICANT: Oleen, David R
APPLICANT: Chang, Robert
APPLICANT: Chishollin, Hugh
APPLICANT: Chishollin, Hugh
APPLICANT: Chishollin, Genald A.
APPLICANT: Chishollin, Genald A.
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT APPLICATION NUMBER: 60/084,828
PRIOR PILLING DATE: 1998-04-10
PRIOR PILLING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 11
SOFTHARE: PATENTIN Ver. 2.0
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Pred. No. 1.6e-141;
1; Mismatches 0; Indels 0
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Sequence 21, Application US/09331347C

Patent No. 6617431

; GENERAL INFORMATION:
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                                                                       FDVGPVCFL 1461
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                                              303 FDVGPVCFL 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1461
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-289-578-9
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ASSUBILITION OF STATE APPLICATION US/09570573

Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

SERIEMATION: Bonde, Martin

TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: In Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS: Darby & Darby PC

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1092 YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGXRKNPARTCRDLKMCHSDWKSGEYW 1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.9%; Score 1670.5; DB 2; Best Local Similarity 98.7%; Pred. No. 2.1e-139; Matches 306; Conservative 0; Mismatches 3; 1
                     APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: GOGOLIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMULCATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFRAX: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                            TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acide
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GFDVGPVCFL 311
    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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US-09-500-811-18

US-09-500-811-18

Sequence 18, Application US/09500811

Patent No. 6323314

GENERAL INFORMATION:

APPLICANT: Oviet, Per APPLICANT: Oviet, Per APPLICANT: Or INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:

ADDRESSER: BOS Third Avenue

STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1032 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSPAGFDFSFLPQPPQEKAHKGGRY 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                        Length 1341;
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STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Vergion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                 Score 1670.5; DB 2
Pred. No. 2.1e-139;
0; Mismatches 3;
                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                  TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.9%;
Best Local Similarity 98.7%;
Matches 306; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
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STREET: 805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino
TOPOLOGY: li
                      CITY: New STATE: Ne COUNTRY:
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Patent No. 635542

GENERAL INFORMATION:

APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1032 NGLPGPIGFPGFPGFRGRIGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQFRAHKGGRY 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFEYGGOGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 1341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 1670.5; DB 2
98.7%; Pred. No. 2.1e-139;
iive 0; Mismatches 3;
                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATCHNEY/AGENT INFORMATION:
NAWE: GOGOZIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKEY NUMBER: 29,714
TELECOMMUCATION INFORMATION:
TELECHONE: 212-527-7700
TELEFAX: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                                                                                        TELEFAX: 212-753-6237
TELEX: 23667
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1341 amino acide
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 98.7
Matches 306; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1332 GFDVGPVCFL 1341
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US-09-548-608-18
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1032 NGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHKGGRY 1091
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                                                                                                                                                 ZIP: 10022

MEDIUM TYPEN FORM:
MEDIUM TYPEN Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
97.9%; Score 1670.5; DB 2
Best Local Similarity 98.7%; Pred. No. 2.1e-139;
Matches 306; Conservative 0; Mismatches 3;
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGORIS, Adda C
REGISTRATION NUMBER: 29,714
REPREDENCE/DOCKET NUMBER: 4305/C
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLAGEN ALPHA 1 (I)
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1341 amino acids
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New York
: New York
RY: USA
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TELECOMMUNICATION INFORMATION
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
      REFERENCE/DOCKET NUMBER:
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1407 EFGVDIGPVCFL 1418
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STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
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Patent No. 6110689
GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QFEYGGGGSDPADVAIQLTFLRIMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSN 180
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                                                                                                                                                                                                  ; OTHER INFORMATION: DESCRIPTION Of Artificial Sequence: SEQUENCE; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS US-09-029-348-14
                                                                                                                                                                                                                                                                                        Length 250;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DEAPHY DISPRIED TO COMPUTER: DATE OF COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                      Query Match 78.9%; Score 1346; DB 2; Best Local Similarity 99.6%; Pred. No. 1.4e-111; Matches 249; Conservative 1; Mismatches 0;
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348;
CURRENT FILING DATE: 1998-05-07;
CURRENT FILING DATE: 1998-05-07;
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
FENGTH: 250
TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR APPLICATION DATA
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFDVGPVCFL 250
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STATE: New York
COUNTRY: USA
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US-08-963-825-20
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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYWIDPNOGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 SNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SNGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPSAGFDFS-FLPQPPQBKAHDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RYYRADD-ANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSG
                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1418;
                                                                                                                                                                                                                                                                                                                                                                                         55; Indels
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                                                                                                                                                                                                                                                                                                                                     Query Match 71.1%; Score 1213.5; DB Best Local Similarity 68.3%; Pred. No. 8.9e-99; Matches 213; Conservative 41; Mismatches 55
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; Sequence 20, Application US/09500811
; Patent No. 6323314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goviet, Per
APPLICANT: Bonde, Martin
ITTLE OF INVENTION: in Body Flui
ITTLE OF INVENTION: Method and ITTLE OF INVENTION: Disorders As
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                  ORGADALIO.
IMMEDIATE SOURCE:

"TONE: COLLAGEN - ALPHA 1 (II)
TELEK: 236687
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1418 amino acids TYPE: amino acid TOPOLOGY: linear
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FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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Sequence 20, Application US/09570573

Batent No. 6342361

GENERAL INFORMATION:
APPLICANT: Qviet, Per
APPLICANT: Qviet, Per
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: in Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1108 ANGIPGPPGPRGRSGETGPAGPPGPPGPPGPPGPPGPGPGIDMSAFAGLGPREKGPDFL 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 EYWIDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKWWYISKNPKDKRHVWFGESMTD 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1213.5; DB 2;
; Pred. No. 8.9e-99;
41; Mismatches 55;
                                       ATTORNEY JAGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-53-6237
TELEFAX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
TYPE: amino acid
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                  i IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
US-09-500-811-20
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STREET: 805 Third Avenue
CITY: New York
STATE: New York
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EFGVDIGPVCFL 1418
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.3
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 EFGFDVGPVCFL 311
                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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US-09-570-573-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1407
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Sequence 20, Application US/09548608

GENERAL INFORMATION:

APPLICANT: Qvist, Per

APPLICANT: Bonde, Martin

TITLE OF INVENTION: A method for Assaying Collagen Fragments

TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for C

TITLE OF INVENTION: method and Use of the Method to Diagnose the TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.1%; Score 1213.5; DB Best Local Similarity 68.3%; Pred. No. 8.9e-99; Matches 213; Conservative 41; Mismatches 55
                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/187,319
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 6090ziā Adda C.
RAGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELEFAK: 212-527-7700
TELEFAK: 212-53-6237
TELEFAK: 236697
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                  APPLICATION NUMBER: US/09/570,573
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IMMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
US-09-570-573-20
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1418 amino acids
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1407 EFGVDIGPVCFL 1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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Texas
USA
                                                                                                                                                                                77210
                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.1%; Score 1213.5; DB 2; Length 1418; 68.3%; Pred. No. 8.9e-99; tive 41; Mismatches 55; Indels 3;
                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                   NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLAGEN -ALPHA 1 (II)
                                                                       ZIP: 10022
COMPUTER READBLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                              TELEX: 236687
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
ADDRESSEE: Darby & Darby STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1418 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1407 BFGVDIGPVCFL 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.34
Matches 213; Conservative
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                         New York
: New York
RY: USA
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                                                         COUNTRY: UR
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61 RYYRADDA-NVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 GFQFEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SNGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPGPPSAGFDFS-FLPQPPQEKAHDGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.7%; Score 1206.5; DB 1; Length 1442; 67.6%; Pred. No. 3.8e-98; ive 45; Mismatches 53; Indels 3;
                                                                                                                                                                                                                                                                                     COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: EIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION NUMBER: US 08/199,780
FILING DATE: 30-SEP-1994
ATTOKNEY/AGENT INPORMATION:
NAME: PATKET, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/CONFUT NUMBER: 32,165
REJERRANICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (713) 789-2679
    APPLICANT: Goldstein, occordant APPLICANT: Lin, Wishan
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: FOR STIMULATING BONE CELLS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
Roessler, Blake J.
Goldstein, Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1442 amino acids
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1431 EFGVDIGPVCFL 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: siz
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RESULT 14 PCT-US95-02251-12

US-08-316-650-12
; Sequence 12, Application US/08316650
; Patent No. 2942496
; GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey

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122 WIDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGF 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFS-FLPQPPQEKAHDGGRY
                                                                                                                                                                                                       APPLICANT: POOLE, Anthony R.
APPLICANT: Hollander, Aathony P.
APPLICANT: Hollander, Aathony P.
APPLICANT: Hollandurst, R. C.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

70.4%; Score 1201.5; DB 2; Length 1418;
Best Local Similarity 68.1%; Pred. No. 1e-97;
Matches 211; Conservative 40; Mismatches 56; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

SOFTWARE PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,999
FILING DATE: 22-JAN-1998
CLASSIFICATION 14335
PRIOR APPLICATION NUMBER: US 08/448,501
APPLICATION NUMBER: US 08/448,501
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATE: US-1992
ATPONEY/AGENT INPOMBER: US 07/984,123
                                                                                                                                                                                                                                                                                                                                                                                                 E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 032931/0212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human Type II Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             Sequence 1, Application US/09010999
Patent No. 6132976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1418 amino acids
     1431 EFGVDIGPVCFL 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3000 K SICITY: Washington STATE: D.C.
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                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                            METHODS AND COMPOSITIONS FOR STIMULATING BONE CELLS
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                                                                                                                                                                                                                                                                                                                                                           COMPUTER KEALMALLE FOUR
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0251
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION OF STEP-1994
CLASSIFICATION WUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
CLASSIFICATION NUMBER: 32,165
RESERENCE/DOCKET NUMBER: 32,165
REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                       Arnold, White & Durkee
Sequence 12, Application PC/TUS9502251
GENERAL INFORMATION:
APPLICANT:
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TELEFAX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TWATH: 1442 amino acids
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Best Local Similarity 67.6
Matches 211; Conservative
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                                                                            TITLE OF INVENTION: ME
TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                    CITY: Houston
STATE: Texas
COUNTRY: United
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ор	1289 HFSYGDDNLAPNTANV(	1289 HFSYGDDNLAPNTANVQMTFLRLLSTEGSQNITYHCKNCIAYLDEAAGNLKKALLIQGSN 1348	48
à	242 EIEIRAEGNSRFTYSV7	242 BIBIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEF 301	1
g G	1349 DVEIRAEGNSRFTYTAI	1349 DVEIRAEGNSRFTYTALKDGCTKHTGKWGKTVIEYRSQKTSRLPIIDIAPMDIGGPEQEF 1408	80
à	302 GPDVGPVCFL 311		
q	1409 GVDIGPVCFL 1418		

³⁰² GPDVGPVCFL 311 | |:||||| 1409 GVDIGPVCFL 1418

Search completed: April 26, 2006, 16:18:00 Job time: 24.4086 secs

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RESULT 2
US-10-677-877A-14
; Sequence 14, Application US/10677877A
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Sequence 14, Appl
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                                                                                                                                              April 26, 2006, 16:17:23 ; Search time 64.095 Seconds (without alignments) 2027.381 Million cell updates/sec
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(cgu2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
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): /cgu2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
(cgu2_6/ptodata/1/pubpaa/USOA_PUBCOMB.pep:*): /cgu2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-677-877A-14
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US-10-734-564-79
US-10-734-564-79
US-10-734-564-79
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US-10-734-794-114
US-10-78-792-114
US-10-357-851-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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No.
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Sequence 2, Application US/10677877A

Sequence 2, Application US/10677877A

Rubication No. US20050202537A1

GENERAL INFORMATION:

APPLICANT: Libraig, Peng; GenHunter Corporation

TITLE OF INVENTION: Receptor analogs and biologically active fusion proteins

TITLE OF INVENTION: Receptor analogs and biologically active fusion proteins

TITLE OF INVENTION: NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

SEQ ID NOS: 16

SEQ ID NOS: 16

LENGTH: 311
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                                                                        US-10-402-072A-8

US-10-106-698-6367

US-10-106-698-6367

US-10-679-811

US-10-677-877A-12

US-10-677-877A-8

US-10-677-877A-8

US-10-677-877A-4

US-10-677-877A-4

US-10-678-877A-4

US-10-678-877A-4

US-10-678-877A-4

US-10-678-877A-4

US-10-678-126-139

US-10-468-091-6

US-10-468-091-6
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US-10-677-877A-10
US-10-677-877A-10
US-10-677-877A-10
Publication No. US20050202537A1
GENERAL INFORMATION
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: Teceptor analogs and biologically active fusion proteins
TITLE REFERENCE: 03-052-PL
CURRENT APPLICATION UNDER: US/10/677,877A
CURRENT FILING DATE: 2003-10-02
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                                                                                                    FQFEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGS
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APPLICANT: Bard St. Croix
APPLICANT: Bert Vogelstein; APPLICANT: Kenneth Kinzler
                                                                                                                                                                                                                                                             FGFDVGPVCFL 311
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Publication No. US20050202537A1
GENERAL INFORMATION:
APPLICANT: Liang, Peng; GenHunter Corporation
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 14
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TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
PILE REFERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 16
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100.0%; Pred. No. 5.2e-130;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                            Matches 311; Conservative
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Best Local Similarity 100.
Matches 311; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                               US-10-677-877A-14
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US-10-171-311-36

Sequence 36, Application US/10171311

Publication No. US2003008727041

Sequence 36, Application US/10171311

Publication No. US2003008727041

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Chen, Yan

APPLICANT: Ghat, Yan

APPLICANT: Ghat, Karen

APPLICANT: Ganatax, Shubhangi

APPLICANT: Ganavarapu, Manjula

APPLICANT: Ganavarapu, Manjula

APPLICANT: Ganavarapu, Manjula

APPLICANT: Hoersh, Sebastian

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY

TITLE OF INVENTION: OF CERVICAL CANCER

TITLE OF PRICE APPLICATION NUMBER: US 60/298,159

PRIOR APPLICATION NUMBER: US 60/298,159

PRIOR PELING DATE: 2001-06-13

PRIOR PELING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/335,936

PRIOR APPLICATE: AND METHODS FOR THE APPLICATION NUMBER: US 60/335,936

| RANDRER OF SEQ ID NOS: 238

| SOPTWARE: PastSEQ for Windows Version 4.0

| LENGTH: 1464
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                                                                                                           1156 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEXAHDGGRY 1215
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            0; Mismatches
            Conservative
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US-10-171-311-36
            Matches 309;
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| Sequence 159, Application US/10060036
| Publication No. US20030073144A1
| GENERAL INPORMATION:
| APPLICANT: Kalos, Michael D. | APPLICANT: Lodges, Michael J. | APPLICANT: Persing, David H. | APPLICANT: Hepler, William T. | APPLICANT: AND DIAGNOSIS OF PANCREATIC CANCER | TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CANCER | CURRENT APPLICATION NUMBER: US/10/060,036 | CURRENT FILIATION DIAGNOSIS OF SEQ ID NOS: 4560 | SOFTWARE FESTSOR for Windows Version 4.0 | SEQ ID NO 159 | SEQ ID NO 159 | LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%; Score 1698; DB 3; Length 1464; 100.0%; Pred. No. 5.8e-129; ive 0; Mismatches 0; Indels 0
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TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT PELLING NUMBER: 08/99/918,715
CURRENT FILING DATE: 2001.08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
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Matches 309; Conservative
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CORGANISM: Homo sapiens
US-10-060-036-159
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-918-715-261
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Zhao, Xumei
Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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Best Local Similarity 100.0%; Pred. No. 5.8e-129;
Matches 309; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                    Sequence 2, Application US/10149352
| Sequence 2, Application US/10149352
| Publication No. US2003010505A1
| GENERAL INFORMATION:
| APPLICANT: Beri, Rajinder
| TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
| TILLE REFERENCE: 06275-254051
| CURRENT APPLICATION NUMBER: US/10/149,352
| CURRENT FILING DATE: 2002-06-10
| PRIOR PILING DATE: 2000-12-12
| PRIOR FILING DATE: 1999-12-15
| PRIOR FILING DATE: 1999-12-15
| RAPOR APPLICATION NUMBER: GB 9929487.8
| PRIOR FILING DATE: 1999-12-15
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: PatentIN Ver. 4.0
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ORGANISM: Homo sapiens
US-10-149-352-2
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US-10-177-293-65
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APPLICANT: Mondhan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Meric, Funda
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILLE REFERENCE: MIL NOBBER: US/10/177,293
CURRENT PILLING DATE: 2002-06-21
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99.5%; Score 100; Double 129; Best Local Similarity 100.0%; Pred. No. 5.8e-129; Matches 309; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILING DATE: 2001-06-21
PRIOR PLILING DATE: 2001-06-21
PRIOR PLILING DATE: 2001-06-27
PRIOR PLILING DATE: 2001-06-27
PRIOR PLILING DATE: 2001-07-18
PRIOR PILING DATE: 2001-07-18
PRIOR PRILING DATE: 2001-09-25
PRIOR PLILING DATE: 2001-09-25
PRIOR PLILING DATE: 2002-05-5
PRIOR PLILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 65
LIENGRADE THANG DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 65
LIENGRADE THANG DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 65
                                                   Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Myer, Vic
Wang, Youzhen
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RESULT 10 US-10-301-822-28

; Sequence 65, Application US/10177293; Publication No. US20030124128A1; GENERAL INFORMATION: APPLICANT: Lillie, James

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; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-79
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                                                                        APPLICANT: MILEGRILIUM FLAILSCONTING FAILSCONTING FAILSCONTING FAILSCONTING FAILSCONTING FAILSCONTING FAILSCONTING FAILSCONTING GUILLEMETE, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: ThiboGeau, Stephen N.
APPLICANT: ThiboGeau, Stephen N.
TITLE OF INVENTION: NETHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
FILE REFERENCE: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US (0/339, 971
FRIOR FILING DATE: 2001-11-10
PRIOR FILING DATE: 2002-03-05
SOFTWARE: FASESSE OF WINDOWS VERSION 4.0
SEQ ID NOS : 228
LENGTH: 1464
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99.5%; Score 1698; DB 4; Length 1464;
Best Local Similarity 100.0%; Pred. No. 5.8e-129;
Matches 309; Conservative 0; Mismatches 0; Indels 0
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Sequence 79, Application US/10734564

Sequence 79, Application US/10734564

Publication No. US20040157278A1

GENERAL INFORMATION:

TITLE OF INVENTION: Detection Methods Using TIMP1

TITLE OF INVENTION: Detection Methods Using TIMP1

FILE REFERENCE: 1657/2012

CURRENT PPLICATION NUMBER: US/10/734,564

CURRENT FILING DATE: 2003-12-12

NUMBER OF SEQ ID NOS: 138

SEQ ID NO 79
Sequence 28, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
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1456 FDVGPVCFL 1464
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US-10-301-822-28
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Query Match 99.5%; Score 1698; DB 4; Length 1464; Best Local Similarity 100.0%; Pred. No. 5.8e-129; Matches 309; Conservative 0; Mismatches 0; Indels 0
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Sequence 261, Application US/10474794;
Bublication No. US20040213793A1;
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor;
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS;
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261
LENGTH: 1464
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Best Local Similarity 100.0
Matches 309; Conservative
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CRGANISM: Homo sapiens
US-10-474-794-261
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Publication No. US20040253606A1

Sequence 2289, Application US/10723860

Publication No. US20040253606A1

GARBEAL INFORMATION:

APPLICANT: Aiiz Natasha

APPLICANT: Zlotnik, Albert

ITILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

ITILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REPREBENCE: 05802.0193.NPUS01

CURRENT APPLICATION NUMBER: 10710.103.0197.0197.39

CURRENT FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-11-26

NUMBER OF SEQ ID NOS: 8339

SOSTWARE: PatentIn version 3.2
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1396 IEIRAEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 1455
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1276 IDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 1335
                                                    IDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 182
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100.0%; Pred. No. 5.8e-129;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 309; Conservative
                                                                                                                                                                                                FDVGPVCFL 1464
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CORGANISM: Homo sapiens
US-10-723-860-2289
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US-10-852-335A-157
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123 IDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 182
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TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumors of Glial Origin FILE REPERENCE: P5103R1-US
CURRENT APPLICATION NUMBER: US/10/852,335A
CURRENT FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 60/548,299
PRIOR APPLICATION NUMBER: US 60/473,238
PRIOR PILING DATE: 2003-02-27
PRIOR PILING DATE: 2003-05-23
NUMBER OF EQ ID NOS: 190
SEQ ID NO 157
LENGTH: 1464
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APPLICANT: Brad St. Croix

APPLICANT: Brad St. Croix

APPLICANT: Brad St. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Bert Vogelstein

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: US/09/918,715

PRIOR APPLICATION NUMBER: 60/222,599

PRIOR PILING DATE: 2001-08-02

PRIOR PILING DATE: 2000-08-02

PRIOR PLILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-01

PRIOR FILING DATE: 2000-08-11

PRIOR PILING DATE: 2000-08-11

TRUEST PRI TATES: PRI TRUEST TATEST TATEST PRI TATE
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Best Local Similarity 100.0%; Pred. No. 5.8e-129;
Matches 309; Conservative 0; Mismatches 0; Indels
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US-10-852-335A-157
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US-10-979-159-261
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US-10-979-159-261
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1156 NGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPGEXAHDGGRY 1215
                            3 NGLPQPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGAGFDF9FLPQPPGEKAHDGGRY
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Query Match 99.5%; Score 1698; DB 5; Length 1464; Best Local Similarity 100.0%; Pred. No. 5.8e-129; Matches 309; Conservative 0; Mismatches 0; Indels 0;
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915, App 910, App 913, App 41, Appl 27, Appl 27, Appl 19, Appl 10, Appl 10, Appl 20, Appl 34, Appl 34, Appl 2106, Appl 34, Appl 34, Appl 4, Appl 4, Appl

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Perfect score:

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE:
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: D0185 PCT
CURRENT PAPLICATION NUMBER: US/10/501,035
CURRENT PILING DATE: 2004-07-09
PRIOR RPPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PATCHIN VERSION 3.2
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 331
LENGTH: 1464
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US-10-995-561-915
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US-10-995-561-913
US-11-124-368A-329
US-11-124-368A-329
US-11-202-057-27
US-11-202-057-27
US-11-202-057-10
US-11-202-057-10
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ORGANISM: Homo sapiens
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Sequence 28, Appl
Sequence 243, Appl
Sequence 1096, Ap
Sequence 344, App
Sequence 318, App
Sequence 918, App
Sequence 918, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 1182, Appl
Sequence 1182, Appl
Sequence 1182, Appl
Sequence 1184, Appl
Sequence 911, Appl
                                                                                                                                                                            April 26, 2006, 16:18:13; Search time 12.2616 Seconds (without alignments) 1153.484 Million cell updates/sec
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1 RSNGLPGPIGPPGPRGRTGD......LDVGAPDQEFGFDVGPVCFL
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(c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
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TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Miliedel, Stephen N.
APPLICANT: METHODE FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: METHODS FOR IDENTIFICANTION: TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029PZRNM
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-07-21
PRIOR FILING DATE: 2002-11-21
PRIOR PELING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 228
SEQ ID NOS: 228
SEQ ID NOS: 228
SEQ ID NOS: 228
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Pred. No. 2.7e-132;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                        ; Sequence 28, Application US/11186284
; Publication No. US20050266493A1
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
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Publication No. US20060003954A1
GENERAL INFORMATION:
APPLICANT: Berl, Rajinder
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Best Local Similarity 100.
Matches 309; Conservative
     1456 FDVGPVCFL 1464
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US-11-186-284-28
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TYPE: PRT
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US-11-021-603-2
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1276 IDPNOGCNI.DAIKVFCNMETGETCVYPTOPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 1335
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APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 786.CIP4CN
CURRENT APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR PRILING DATE: 2002-11-08
PRIOR PRILING DATE: 2001-01-25
PRIOR PLILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-08-03
TILE REPERENCE: 06275-254US1
CURRENT APPLICATION NUMBER: US/11/021,603
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/149,352
PRIOR PILING DATE: 2002-06-10
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 4.0
SEQ ID NO 2
LENGTH: 1464
TYPE: PRT
CREATE: 1464
TYPE: PRT
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APPLICANT: Tang, Tom
APPLICANT: Liu, Chenghua; APPLICANT: Asundi, Vinod; APPLICANT: Chen, Rui-hong; APPLICANT: Wang, Ziachong B.
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Sequence 1096, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat. Ivan

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

CURRENT FILES OF 100 NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR PPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt_SEQ_genes Version 1.0

SEQ ID NO 1096

LENGTH: 1467
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                                                                                                                                                                                                                                                                                                                      3 NGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPSAGFDPSFLPQP
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-17
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 944
SEQ ID NO 243
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|456 FDVGPVCFL 1464
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CORGANISM: Homo sapiens
US-11-000-463-243
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1159 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY 1218
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                                                              YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGBYW 122
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                                                                                    YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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Publication No. US20060084066A1

GENERAL INFORMATION:
APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: Patentin version 3.2

SEQ ID NO 344

LENGTH: 1453

TYPE: PRT

ORGANISM: rat
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1445 MDIGPACFV 1453
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US-10-784-004-344
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RESULT 7 US-10-784-004-434

3 NGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRY

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1205 YRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW 1264
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90.9%; Pred. No. 1.9e-123;
iive 16; Mismatches 12;
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US-11-202-057-3
US-11-202-057-3
Sequence 3, Application US/11202057
Publication No. US20060051794A1
GENERAL INFORMATION:
APPLICANT: TSAI, SHIH-FENG
APPLICANT: LIU, YU-FEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9
Matches 281; Conservative
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1445 MDIGPACFV 1453
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US-10-784-004-950
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                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                              Length 1453;
                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                              93.2%; Score 1591; DB 6;
90.9%; Pred. No. 1.9e-123;
tive 16; Mismatches 12;
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Publication No. US20060084066A1
GENERAL INFORMATION:
APPLICANT: Biogen Idec
TITLE OF INVENTION:
FILE REPERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004;
CURRENT PILING DATE: 2004-02-20;
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2;
SEQ ID NO 918
Sequence 434, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; TITLE CAT: Biogen idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT PILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
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Best Local Similarity 90.94
Matches 281; Conservative
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1445 MDIGPACFV 1453
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Best Local Similarity
                                                                                                                                                   SEQ ID NO 434
LENGTH: 1453
TYPE: PRT
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US-10-784-004-918
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US-10-784-004-434
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US-10-784-004-918
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TYPE: PRT
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1145 NGLPGPIGPPGPRGRTGDSGPAGPPGPPGPPGPPSGGYDFSFLPQPPQEKSQDGGRY 1204
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123 IDPNQCCNLDAIKVPCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGPQ
                                                                                                     183 FEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE
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US-11-202-057-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQ 299
                                                                                                                                                                                                                                                                 2 SNGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPGPPSAGFDFS-FLPQPPQEKAHDGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/11202057

Publication No. US20060051794A1

GENERAL INFORMATION:

APPLICANT: TSAI, SHIH-FENG

APPLICANT: CHEN, WEI-MING

TITLE OF INVENTION: MITATIONS AND COMPOSITIONS RELATING TO COL2A1 GENE

TITLE OF INVENTION: MITATIONS AND OSTEONECROSIS

TITLE OF INVENTION: MITATIONS AND OSTEONECROSIS

FILE REFERENCE: 08842.0011-00000

CURRENT APPLICATION NUMBER: 08/11/202,057

CURRENT FILING DATE: 2004-08-18

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTIN VEY: 3.2

SEQ ID NO 5.
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APPLICANT: CHEN, WEI-MING
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO COL2A1 GENE
TITLE OF INVENTION: MUTATIONS AND OSTEONECROSIS
FILE REPERENCE: 08842.0011-00000
CURRENT APPLICATION NUMBER: US/11/202,057
CURRENT FILING DATE: 2005-08-12
PRIOR PRILNG DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PATENTIN Ver. 3.2
SEQ ID NO 3
LENGTH: 1487
                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                DB 7; Length 1487;
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68.3%; Pred. No. 3.4e-92;
ive 41; Mismatches 55;
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Best Local Similarity 68.3'
Matches 213; Conservative
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                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-202-057-3
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ORGANISM: Homo sapiens
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SNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGAGFDFS-FLPQPPQEKAHDGG

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SNEIBIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQ 299
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; Publication No. US20060051794A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIU, YU-FEN
TITLE OF INVENTION: METHONS AND COMPOSITIONS RELATING TO COLLAI GENE
TITLE OF INVENTION: MITATIONS AND COMPOSITIONS RELATING TO COLLAI GENE
TITLE OF INVENTION: MITATIONS AND COMPOSITIONS RELATING TO COLLAI GENE
TITLE OF INVENTION: MITATIONS AND COSTONERROR PERLOR NOT SOOF 00-1
CURRENT PELING DATE: 2005-00-1
PRIOR APPLICATION NUMBER: 60/602,319
PRIOR FILING DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 7.00
                                                                                                                                                                                                                                                           GFQFEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKG
                                                                          RYYRADD-ANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSG
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|476 EFGVDIGPVCFL 1487
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Best Local Similarity 68.3%
Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.0%; Score 1024; DB 7;
Best Local Similarity 58.4%; Pred. No. 1.5e-76;
Matches 181; Conservative 45; Mismatches 68;
              PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 1366
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Publication No. US20050255114A1
GENERAL INFORMATION:
2005-07-21
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1356 FFVDIGPVCF 1365
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CRGANISM: Homo sapiens
US-10-821-234-964
                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo Sapiens
US-11-186-284-31
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Publication No. US20050266493A1

GENERAL INPORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Howerned J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

FILE REFERENCE: MPMO1-029P2RNM

CURRENT APPLICATION NUMBER: US/11/186,284
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| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat. Ivan
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Andarami, Susan
| APPLICANT: Tang, Y. Tom
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| FILE REFERENCE: 8218
| CURRENT APPLICATION NUMBER: US/10/821,234
| CURRENT APPLICATION NUMBER: US 60/462,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| PRIOR FILING DATE: 2003-04-07
| WUMBER OF SEQ ID NOS: 1704-07
| SGO ID NO 1431
| LENGTH: 1366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 RAD---DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%; Score 1024; DB 6; Length 1366; 58.4%; Pred. No. 1.5e-76; tive 45; Mismatches 68; Indels 16
  1476 EFGVDIGPVCFL 1487
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Best Local Similarity 58.4<sup>†</sup>
Matches 181; Conservative
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1356 FFVDIGPVCF 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1431
                                                                      RESULT 13
US-10-821-234-1431
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmal, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT FILING DATE: 2004-04-07
PRIOR PILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 964
LENGTH: 1166
                                                            240
                                                                                                                                               241 NEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQE 300
                                                                                     181 FOFEYGGGGSDPADVAIQLTFLRLMSTEASONITYHCKNSVAYMDQQTGNLKKALLLKGS
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Best Local Similarity 60.3%; Pred. No. 2.1e-75;
Matches 191; Conservative 40; Mismatches 76;
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Search completed: April 26, 2006, 16:20:39 Job time : 13.2616 secs

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AR397575 Sequence

S64596 COLIAL=Type
AX146420 Sequence
XX146420 Sequence
XX16426 Sequence
XX164216 Sequence
XX16423 Sequence
XX19339 Sequence
XX19339 Sequence
XX19339 Sequence
XX19345 Sequence

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Run on:

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Astle, J.H., Boardman, L.A., Bugart, L.J., Burgess, C.C., Catino, T.J., Dwivedi, P., Huntress, M., Johnson, K.A., Lewis, M.E., Maimonis, P.J., Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and Molino, G.A.

Detection methods using TIMP 1 for colon cancer diagnosis
Patent: EP 1439393-A 12 21-JUL-2004;

Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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|mol_type="unassigned DNA"
|db_xref="taxon:9606"
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Sequence 12 from Patent EP1439393.
CQ833976
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CQ833976
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CS06950 Sequence
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AX330012 Sequence
AX3330557 Sequence
AX33330 Sequence
AX33330 Sequence
AX13130 Sequence
AX11312 Sequence
AX776245 Sequence
AX776245 Sequence
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AX776246 Sequence
                                                                                                         April 27, 2006, 17:15:53 ; Search time 4395.68 Seconds (without alignments) 9970.316 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                             nucleic search, using sw model
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AX393330
AX1302
AX11302
AX411302
AX411302
AX71221
AX776246
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PAT 29-JUL-2004

CCGTGACCTCAAGATGTGCCACTCTGAAGAGTGGAGAGTACTGGATTGACCCCAA 196

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
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                                                                                                                                                                  CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
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Munnes, M. and Bojar, H.
Methods and kits for investigating cancer
Patent: WO 2005040414-A 153 06-MAY-2005;
Bayer HealthCare AG (DE)
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/mol_type="unassigned DNA"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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100.0%; Pred. No. 1.3e-111;
iive 0; Mismatches 0; Indels
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Methods and kits for investigating cancer
Batent: EP 1522594-A 153 13-APR-2005;
Bayer HealthCare AG (DE)
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Sequence 153 from Patent BP1522594.
CS063169
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/db_xref="taxon:9606"
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PGLPGPSGEPGKGCPSGASGERGPPGPMGPPGLAGPPGESGREGAPAAEGSPGRDGSP
GAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPVGPVGARGPAG
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PQEKAHDGGRYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDL
KMCHSDWRSGEYWIDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKD
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QQTGNLKKALLLKGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSR
LPIIDVAPLDVGAPDQEFGFDVGFVCFL"
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100.0%; Pred. No. 1.2e-111;
:ive 0; Mismatches 0;
                                                                                                                                                                                 /note="unnamed protein product" /codon_start=1
                                                                                       1. .6728
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
120. .4514
Beri,R.
Antisense oligonucleotides
Patent: WO 0144455-A 1 21-JUN-2001;
                                                                      Location/Qualifiers
                                                       AstraZeneca AB (SE)
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Hominidae; Homo.
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Sequence 1 from Patent W00144455.
AX167114 GI:14596602
   /db_xref="taxon:9606"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Cancer gene determination and therapeutic screening using signature
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
            317 GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
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97.4%; Score 751; DB 6; Length 6728;
Best Local Similarity 100.0%; Pred. No. 1.2e-111;
Matches 751; Conservative 0; Mismatches 0; Indels
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Patent: WO 0194629-A 1066 13-DEC-2001;
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AX330557
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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.larity 100.0%; Pred. No. 1.2e-111;
Conservative 0; Mismatches 0; Indels
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Patent: WO 0194629-A 521 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini,
Hominidae; Homo.
                                                                            TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCACCACAAGAGCCTGAG
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Endothelial cell expression patterns
Patent: WO 0210217-A 260 07-FEB-2002;
97.4%; Score 751; DB 6; Le Similarity 100.0%; Pred. No. 1.2e-111; Conservative 0; Mismatches 0;
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Sequence 260 from Patent WO0210217.
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GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG 4135
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                                                                                     CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG 256
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                        CGTGTACCCCCACTCAGCCCCAGTGTGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAA
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                              CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGTACTGGATTGACCCCAA
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Avalon Pharmaceuticals (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 1.2e-111;
iive 0; Mismatches 0;
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          Location/Qualifiers
1. 6728
1. Coganism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 Johns Hopkins University (US)
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                                                                                                                Best Local Similarity 100.
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Chordata, Craniata, Vertebrata, Euteleostomi;
Buarchontoglires, Primates; Catarrhini;
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                                                                      and Vockley, J.G.
                                                                                                                                                                                                                                                                                              Length 6728;
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Location/Qualifiers
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Chu,M.L., de Wet,W., Bernard,M. and Ramirez,P.
Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter structure, Alul repeats, and polymorphic transcripts 2857713.
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1 (bases 1537 to 3803)
Bernard, M.P., Chu, M.L., Myers, J.C., Ramirez, F., Eikenberry, E.F. and
                                 PRI 07-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-JUL-1996) Raymond Dalgleish, Department of Genetics,
University of Leicester, University Road, Leicester, LB1 7RH,
United Kingdom
                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Human pro alpha 1(1) collagen: cDNA sequence for the C-propeptide
                                                                                                                                                                                                                                           Nucleotide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procollagen. Statistical evaluation of structures that are conserved during evolution Biochemistry 22 (22), 5213-5223 (1983)
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Highly conserved sequences in the 3'-untranslated region of the
COLLA1 gene bind cell-specific nuclear proteins
FEBS Lett. 279 (1), 9-13 (1991)
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Blochem. J. 253 (3), 919-922 (1988)
                                 linear
                6728 bp mRNA lin
H.sapiens mRNA for prepro-alphal(I) collagen.
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274615. GI:1418927
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Submitted (122-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research, 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930, Pax:81-438-52-3931)

This work was supported in part by the National Project on Protein structural and Functional Analysis , Ministry of Education, Culture , Sports, Science and Technology of Japan. Totoki Y, Toyoda A, Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABLOUSS97 4721 bp mRNA linear PRI 31-MAR-2005
Homo sapiens mRNA for Collagen alpha 1 chain precursor variant
protein.
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None Title
Published Only in Database (2005)
2 (bases 1 to 4721)
Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S., Ohara,O., Nagase,T. and F.Kikuno,R.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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                       GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
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Pred. No. 7.3e-111;
0; Mismatches 3;
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PE Corporation (NY) (US)
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/db_xref="taxon:9606"
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Location/Qualifiers
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Matches 748; Conservative
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QNGLRYHDRDVWKPEPCRICVCDDNGKVLCDDVICDETKNCPGAEVPEGECCPVCPDGS
ESPTDQETTGVEGPKGDTGPRGPRGPAGPPGRDGIPGQPGLPGPPGPPGPPGPPGLGG
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PGSAGAPGROCLINGLEPEPIGPPGPRGTGDAGPYGPPGPPGPPGPPGPPGPPSTGPP
PGPPGEKAHUGGRYKAADDANVVBRDLEVDTTLKSLSQQI ENIRSPBGSRRNPARTC
RDLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKN
PKOKRHWYGESBMTDGPPSYGQSPDADVAIQLTFLRLMSTRASQNITYHCKNSVA
YMDQTTGNLKKALLLLQGSNEIBIRASGNSRFYSVTVDGCTSHTGAMGKTVIEYKTTK
TSRLPIIDVAPLDVGAPDQEFGFDVGFVCFL
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Center, 1-7-22 Suehiro-cho, Tøurumi, Yokohama 230-0045, Japan.
e-mail: aktanaka@postman.riken.go.jp
URL: http://protein.gsc.riken.go.jp/.
Location/Qualiffeers
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                                                                                                                                                                                                                                                                                    /gene="Collagen alpha 1 chain precursor variant"
/note="Start codon is not identified."
/codon start=1
/evidence=not experimental
/product="Collagen alpha 1 chain precursor variant"
/protein_id="BAD92834.1"
/db_xref="G1:62088774"
                                                                                                                                                                                                                                                      variant"
                                                                                                                                                                       /tissue type="spleen"
/note="this clone is also named as hsk003001786
vector:pBluescriptII SK plus"
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                                                                                                                                                                                                                                                    /gene="Collagen alpha 1 chain precursor
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Pred. No. 7.8e-111;
0; Mismatches 3;
                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="sj06448"
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HUMCGIPA1 3347 bp mRNA linear PRI 01-NOV-1994
Human proalpha 1 (I) chain of type I procollagen mRNA (partial).
K01228
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Bernard, M.P., Chu, M.L., Myers, J.C., Ramirez, F., Bikenberry, B.F. and
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Worlectide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procollagen. Statistical evaluation of structures that are conserved during evolution electronistry 22 (22), 5213-5223 (1983)
Original source text: Human cDNA to human skin fibroblast mRNA.
2625 CGTGTACCCCACTCAGCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                    ccaagecrecaaccregareccarcaaagrcrrcrecaacaregagacregagaccre
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Suppression of polymeric alleles
Patent: WO 03048362-A 16 12-JUN-2003;
College of the Holy and Undivided Trinity of Queen Elizabeth
Location/Qualifiers
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0; Mismatches 4;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens collagen, type I, alpha 1, mRNA (cDNA clone MGC:33668
BC036531
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       2745 CGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCCTGATGTC 2804
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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HN-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:22328091.
                                                                                                                           CACCGAGGCCTCCCCAGAACATCACCTACCACTGCAAGAACAGGGTGGCTACATGGACCA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens
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The human proalpha 1 (1) chain of type I procollagen is compared with those of calf, rat, mouse and chicken and with the proalpha 2 (1) chain from man. Selective pressure during 250,000,000 years of evolution acted more strongly on the proalpha 1 (1) chain than on the proalpha 2 (1) chain. The alpha 2 (1) chain domain as sequences are not as highly conserved as those of the C-propeptide domain of the same chain.
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codon_start=1
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/db_xref="GI:180392"
/db_xref="GDB:G00-119-061"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGGPSGGPSGASGPAGPRSGPPGS
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QQTGNLKKALLLLQGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKTSR
LRIIDVAPLDVGAPDQEFGFDVGHVCFL"
                              Shiraki
           Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Institute for Systems Biology

http://www.systemsbiology.org

contact: amadan@systemsbiology.org

Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Search completed: April 27, 2006, 20:12:52 Job time : 4400.68 secs

DRIGIN

TGATGCCAATGTGGTGGTGCGTGACCTCGAGGTGGACACCCTCAAGAGCCTGAG 17

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Length 4752;

Score 743; DB 8; Length 47 Pred. No. 2.6e-110; 0; Mismatches 5; Indels

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Conservative

Similarity

Query Match Best Local Simi Matches 746;

96.4%;

Abl62729 Colon ade Abl63721 Human Canc Abl92119 Human Tum Abn97451 Gene #394 Abv94755 Human pan Acc50108 Breast ca Acc50108 Breast ca Acc50108 Breast ca Abx72044 Human src Abx72044 Human src Add14744 Human mrc Adv70139 Tumor-ass Ade770139 Tumor-ass Ade87389 Human pan Ads2241 Human cDN Ads81387 Human pan Ade87382 Human pan Ade87383 Human pan Ade87381 Human col

Sequence:

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Searched:

Database

Result

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Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
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construct protein"
/note= "No start codon"
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ABN97455
ABN94755
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ADD14744
ADD65586
ADE87386
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AD52677
AAS22677
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AD587382
ACC46568
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                                         P-PSDB; AEA28571.
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Aea2852 Human alk
Aea28578 Human alk
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Aea2858 Human col
Aea28570 Human sol
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             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                          The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion. to the polypeptide to be trimerized, which in turn is joined in-frame to a signal peptide capable of self-trimerization which is heterologous to the first polypeptide capable of self-trimerization which is heterologous to the first polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of cularyotic cell. Receptor decoys theoretically should have a much ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such carionally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their manners appared a plane of the invention of the human collagen appared to the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 771 BP; 186 A; 247 C; 204 G; 134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 771; DB 14;
100.0%; Pred. No. 2.6e-162;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               contain the glycine-repeat triple helical region.
Claim 14; SEQ ID NO 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Eact Local Similarity 100.0
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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a conspect cell. Receptor decoys, e.g. soluble receptors consisting of cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be used for useful for generating a secreted trimeric fusion protein to be used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
protein secretion; fusion protein; protein activation; collagen I; ss; gene; CD4; gene fusion; mutant.
                                                                                                                CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACAT
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                                                                                                                                                                                                                                                           721 TCGGCTTCGACGTTGGCCCTGTTCCTGTAAACTCCCTCCATCTAGA 771
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Chimeric.
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protein secretion; fusion protein; protein activation; collagen I; ss; gene; Alkaline phosphatase; gene fusion; mutant.

Homo sapiens.

Synthetic. Chimeric.

Human alkaline phosphatase-collagen alpha(I) C-propeptide fusion

U

/product= "Human alkaline phosphatase-collagen alpha(I)
-propeptide fusion protein"
/transl_except= (pos:1536, .1537, aa:Arg)

02-OCT-2003; 2003US-00677877. 04-OCT-2004; 2004WO-US032753

WO2005047850-A2

26-MAY-2005

(GENH-) GENHUNTER CORP.

Liang P;

WPI; 2005-386406/39. P-PSDB; AEA28575.

Location/Qualifiers

Key

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1427
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                                                                                                                                                                                                                                                                                            Score 760; DB 14; Length 1947;
Pred. No. 8.9e-160;
                                                                                                                                                                                                                              Sequence 1947 BP; 497 A; 545 C; 538 G; 367 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 6.2
                                                                                                                                                                                                                                                                                            98.68;
                                                                                                                                                                                                                                                                                                                                                          Matches 760; Conservative
                                                                                                                                                                                                                                                                                                                         Local Similarity
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Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be

Claim 17; SEQ ID NO 7; 47pp; English.

trimerized

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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the colypeptide capable of self-trimerization which is heterologous to the colypeptide capable of self-trimerization which is heterologous to the ciffret polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of cukaryotic cell. Receptor decoys theoretically should have a much conjugate and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much retroally designed soluble trimeric receptor analogs could significantly controlly designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of cursing injections for each patient. The method of the invention may be conserually occurring trimeric ligands. The current sequence is that of the naturally occurring trimeric ligands. The current sequence is that of the human placental alkaline phosphatase (AP)-human collagen alpha(I) conserual includes a mutated BMP-1 recognition site but does not contain contain region.
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7 12 AGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGC ö 98.6%; Score 760; DB 14; Length 2294; 100.0%; Pred. No. 9.2e-160; Sequence 2294 BP; 503 A; 737 C; 676 G; 378 T; 0 U; 0 Other; Best Local Similarity 100.0%; Pred. No. 9.2 Matches 760; Conservative 0; Mismatches 8

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28-JUL-2005 AEA28574;

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                            ACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGGAGTACTGGATTGAC 191
                                                                192 CCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAG
                                                                                                   252 ACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAAC
                                                                                                                                       312 CCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGGATGACCGATGGATTCCAGTTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein secretion; fusion protein; protein activation; collagen I; ss;
gene; Tumor necrosis factor; TNF-RII; gene fusion; mutant.
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/product= "Human soluble TNF-RII-collagen alpha(I)
propeptide T2 fusion protein"
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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a first polypeptide to be trimerized, and introducing the construct into a circ polypeptide to be trimerized, and introducing the construct into a circ polypeptide to be trimerized, and introducing the construct into a confirst polypeptide to be trimerized, and introducing the construct into a confirm the extracellular ligand-binding domain, may be used to intercept a configuration of the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much rationally designed soluble trimeric receptor analogs could significantly increase clinical benefite, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their naturally occurring trimeric ligands. The current sequence is that of the human soluble TNP-RII-human collagen alpha(I) C-propeptide T2 fusion DNA (sTMF-RII-T2) of the invention. The collagen T2 construct includes a matated BMP-I recognition site but does not contain the glycine-repeat
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Pred. No. 1.4e-159;
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04-OCT-2004; 2004WO-US032753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
                                                                                                                                                                                                                                                                                                                                                                                                     protein secretion; fusion protein; protein activation; collagen I; ss; gene; Tumor necrosis factor; TNP-RII; gene fusion.
  CATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGAACTCGGAATTCGGCTTCGACGTTGG
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                                                                                   CCCTGTCTGCTTCCTGTAACTCCCTCCATCTAGA 771
                                                                                                         CCCTGTCTGCTTCCTGTAAACTCCCTCCATCTAGA 963
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/product= "Human soluble TNF-F
propeptide TO fusion protein"
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18. .1718
                                                                                                                                                                                                                                   AEA28576 standard; cDNA; 1734 BP
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P-PSDB; AEA28577.
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Synthetic.
Chimeric.
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                                                                                                                                                            980 TGATGCCAATGTGGTTCGTGACCTCGAGGTGGACACCACCACCTCAAGAGCCTGAG
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                                                                                                                           17 TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCCCTCAAGAGCCTGAG
                                                                                                                                                                                                               197 CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
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                                         Length 1734;
Sequence 1734 BP; 358 A; 598 C; 477 G; 301 T; 0 U; 0 Other;
                                                                                 Indels
                                     97.9%; Score 755; DB 14; L
100.0%; Pred. No. 1.1e-158;
ive 0; Mismatches 0;
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376

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CATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGGAATTCGGCTTCGGCTTGG 2104
                                                    CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACTG 1624
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                                                                                                                                                                                                                                                            GGACAAGAGGCATGCTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
                                                                                                                                                        CGTGTACCCCACTCAGCCCAGTGTGTGTGTGTAAAAAACTGGTACATCAGCAAAAAACCCCAAA
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gene; Alkaline phosphatase; gene fusion.
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                                                                                                                           CGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
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                                                                                                                                                                                                                         "Human soluble CD4-collagen alpha(I)
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                                                                                                                                                                                                                                                    propeptide TO fusion protein"
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                                                                                                                                                   Location/Qualifiers
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/*tag= a
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gene, CD4, gene fusion.
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P-PSDB; AEA28581.
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                                                 Homo sapiens.
Synthetic.
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                                                                                                                                                                            The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the cignal peptide to be trimerized, which in turn is joined in-frame to a colypeptide capable of self-trimerization which is hereologous to the first polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of coly the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of increase clinical benefits, as well as lower the amount or frequency of cuseful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their current sequence is that of the numan placental alkaline phosphatase (AP)-human collagen alpha (I) corpropertide TO fusion DNA (AP-TO) of the invention. The collagen TO construct includes a partial glycine-repeat triple helical region.
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                                                                                      Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 755; DB 14; I Pred. No. 1.2e-158;
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100.0%; Pred. No. 1...
... 0; Mismatches
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Best Local Similarity 100.
Matches 755; Conservative
(GENH-) GENHUNTER CORP.
                                                  WPI; 2005-386406/39
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The invention relates to a novel isolated polymucleotide comprising any of the 235 nucleotide sequences described in the specification. The invention further comprises: an isolated polymucleotide encoding a polypeptide with biological activity, where the polymucleotide hybridizes to one of the 235 novel polymucleotides under stringent hybridization conditions, or having greater than about 99% sequence identity with the novel polymucleotide; a vector comprising a novel polymucleotide; an expression vector comprising the novel polymucleotide; and expression vector comprise the novel polymucleotide; a host cell contains associated with a regulatory sequence that modulates operatively associated with a regulatory sequence that modulates polymucleotide in the host cell; an isolated polymucleotide in the host cell; an isolated polymucleotide in the host cell; an isolated polymucleotide in the novel polymucleotide; a composition comprising the polypeptide and a carrier; an antibody
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                                                                                                                                                                                                      2333 cegaeccreeecaacacacacrearreaaracaacaccaccaacrecceccecceccar 2392
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                                                                      2213 GCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCG
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RESULT 10

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directed against the polypeptide; a method for detecting the novel polymucleotide in a sample; a method for detecting the polypeptide in a sample; a method for detecting the polypeptide in a sample; a method for identifying a compound that binds to the polypeptide; a method for producting the polypeptide; an isolated polypeptide comprising any of the 235 amino acid sequences described in the specification; and a collection of polymucleotides comprising of at least one of the polymucleotides cited above. The polypeptides and polymucleotides of the invention have antiinflammatory, cytostatic, and antimicrobial activities. The novel polymucleotide may be used to treat disorders by gene therapy. The polypeptides and polymucleotides are useful for treating inflammation, leukaemias, nervous system disorders, or infections. This sequence represents one of the 235 novel isolated
                                                                                                                                                                                                                                                                                                                                                                                                                  TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGAGCCTGAG
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Pred. No. 1e-157;
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The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polygeptide see ACCS0076 to ACCS0334 and ABR47386 to ABR47381 in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a patient sample and the normal level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cycostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Zhao X, Meyers RE;
Sahin A, Mills GB;
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of a marker in a patient sample with that in the control non-breast
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Myer V, Wang Y, Xu Y, Zhao X,
Pusztai L, Meric F, Sahin A,
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                                                                                                                                            Human; breast cancer; cytostatic; gene therapy; gene;
                                                                                                              Breast cancer associated cDNA sequence SEQ ID NO:66
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Pred. No. 1.1e-157;
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100.0%; Pred. No. ...
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2001US-0301572P.
2001US-0306501P.
2001US-0325002P.
2002US-0362585P.
             ACC50109 standard; cDNA; 5921
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Mertens M, Monahan JE, M
Bast RC, Hortobagyi GN,
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Best Local Similarity 100.
Matches 751; Conservative
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25-SEP-2001;
05-MAR-2002;
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                        autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; anxylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a cutoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that compression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of turther comprises: a treatment of theumatoid arthritis; identification of turther comprises: a treatment of rheumatoid arthritis; dentification of other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis. The compositions of the invention have the following continuous and treating autoimmune disease or arthritides, such as antigout, antimflammatory, dermatological, and immunosuplatory. The methods and compositions of the present invention are useful for methods and treating autoimmune disease or arthritides, such as themmatoid arthritis, lupus, ankylosing spondylitis, fibrositis, crepresents a DNA sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides; such as treatment of autoimmune diseases or arthritides; such as treatment of autoimmune disease or arthritides; such as the expensent of autoimmune diseases or arthritides; such as the expense or a part or the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is the expense or a proposition of the genes used in the analysis and the expense or the form of a proposition of the genes arthritides. Note: This sequence is the expense or the form of the form of the genes of the control of th
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                                                             Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3836 CCAGCAGATCGAGAACATCCGGAGCCCAGAGGAAGCCGCAAGAAGCCGCAGCCCGCCCGCACCTG
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Pred. No. 1.1e-157;
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100.0%; Pred. No. ...
'... 0; Mismatches
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Matches 751; Conservative
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Query Match 97.4%; Score 751; DB 12; I Best Local Similarity 100.0%; Pred. No. 1.1e-157; Matches 751; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                              736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                     CGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCCCCCAAGTCCTCCCGCCTGCCCAT
                     CGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACAC
                                                                              CGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACAC
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sednence #8
                                                                                    Human colorectal cancer-associated protein coding
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                                                                                                 human; colon cancer; TIMP1; Reg1-alpha; colorectal cancer-associated marker; gene;
                                                                                                                         Homo sapiens
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5921 BP; 1068 A; 1879 C; 1763 G; 1211 T; 0 U; 0 Other;

Sequence

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The present invention relates to a method (M1) for diagnosing breast cancer in a patient. The method comprises comparing the level of cancer in a patient. The method comprises comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating continuation and array for distinguishing between normal and disease tissues comprising two or more probes corresponding to genes selected from ADR99121 and the gene products are polypeptides selected from ADR99121 and the gene products are polypeptides selected from ADR99121 and the gene products are polypeptides selected from ADR99121 and the gene products are polypeptides selected from ADR99122. ADR99121 and diagnosing breast cancer. M2 and the array are useful for diagnosing breast cancer. M2 and the array are useful for distinguishing between normal and disease tissue. M3 is useful
1256 GCAGACTGGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCAACGAGATCGAGATCCG 4315
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with that in a normal patient sample.
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                                                                                                                                                                                                                                                                                                Myerow SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a method for diagnosing colon cancer in an individual, the method involves obtaining a serum sample from the individual and detecting the presence of either TIMP1 or Regl-alpha and an additional colorectal cancer-associated marker. The method of the invention is useful for diagnosing colon cancer in an individual. The present DNA sequence represents a human colorectal cancer-associated protein coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGTGACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGGAGTACTGGATTGACCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing colon cancer in individual, preferably human, by detecting presence of TIMP 1 in sample, where presence of TIMP 1 in sample is indicative of colon cancer in individual.
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Huntress M, Johnson KA, Lewis ME, Maimonis PJ,
er SLA, Thiagalingam A, Thibodeau SN, Molino GA;
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Pred. No. 1.1e-157;
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100.0%; Pred. No. 1.1.
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                       Brown-Shimer SLA, Thiagalingam A,
                                                                                                                                     2002US-0433554P
2003US-0491397P
                                                                                             15-DEC-2003; 2003EP-00257868
                                                                                                                                                                                                         (FARB ) BAYER HEALTHCARE LLC
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hes 751; Conservative
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                                                                                                                                       13-DEC-2002;
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Detecting lineage-specific cells in a biological sample, useful for determining the clinical outcome of a progenitor cell transfer in subject, comprises identifying lineage-specific mRNA in the sample.
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                                                                                                                                                    25-SEP-2003; 2003US-0506221P.
08-OCT-2003; 2003US-0509594P.
                                                                                                                          24-SEP-2004; 2004WO-US031524
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               culture;
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                                                                                                                                                                                                           CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCCAA 196
an anti-cancer agent. M4 is useful for identifying a compound for treating breast cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                  TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAA
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                                                                   Sequence 5921 BP; 1068 A; 1879 C; 1763 G; 1211 T; 0 U; 0 Other;
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                                                                                             97.4%; Score 751; DB 13; Length 5921;
100.0%; Pred. No. 1.1e-157;
tive 0; Mismatches 0; Indels 0
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                                      The invention relates to a method of detecting lineage-specific cells in a biological sample which comprises identifying lineage-specific mRNA in the sample. The methods are useful for determining the clinical outcome of a progenitor cell transfer in a subject, and for identifying or quantifying lineage-specific cells. The present sequence represents a human cDNA that encodes a protein used to identify lineage-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAG
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Disclosure; SEQ ID NO 198; 393pp; English
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CDNA;

standard;

ADZ26572

ADZ26572

Human type I collagen cDNA.

(first entry)

16-JUN-2005

Search completed: April 27, 2006, 19:33:57 Job time : 484.986 secs

Shultzomi 602286109 BP172582 EST00095

170004243

603178681

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

170005322 AGENCOURT 55113737H AGENCOURT CES001271 CR28D04.Y

UNL-P-FN-UNL-P-FN-56095953H AGENCOURT

55113737J 1098545 M

Shultzomi

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AY414729 3492 bp DNA linear GSS 17-DEC-2003
Homo sapiens COLIAl gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 3492)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferritara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.2%; Score 734.2; DB 10; Length 3492; Best Local Similarity 99.6%; Pred. No. 2.3e-165; Matches 736; Conservative 0; Mismatches 3; Indels 0;
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CV674726
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BI916706
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CA976611
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BI181563
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AP414730 Pan trogl
BP172845 BP172845
CN342548 170064249
CV547993 BP172993
CN547993 BP172993
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CN542240 17005321
DR43254 AGENCOURT
CN342328 AGENCOURT
AP577435 GV3-EP053
CN342984 AGENCOURT
AP577435 GV3-EP053
CN3423321 AGENCOURT
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DR768506 ILLUMIGEN
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DN103076 1098161 M
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               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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9b_est4:*
9b_est4:*
9b_est6:**
9b_est7:*
9b_gs82:*
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from embryoid body outgrowths derived from hES cell lines
HI (pl2), H7 (pl2), and H9 (pl2) maintained in feeder-free
conditions."
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Contact: Brandenberger
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, US/
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 762 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.8%; Score 715.6; DB 7; ilarity 99.4%; Pred. No. 5.5e-161; Conservative 0; Mismatches 4;
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 762)
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                                                                                                                                        CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGGAGGTACTGGATTGACCCCAA
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                       TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAG
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17000425072448 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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Hominidae; Homo.

13. (Lease 1 to 1035)
11., W.B. .. Gruber. C., Jessee, J. and Polayes, D.

14. (Lease 1 to 1035)
11., W.B. .. Gruber. C., Jessee, J. and Polayes, D.

15. Ini, M.B. .. Gruber. C., Jessee, J. and Polayes, D.

16. 2010 this sequence version replaced gi:30604612.

17. Contact: Genoscope
17. Genoscope Centre National de Sequencage
18. The Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
18. Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
18. strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
18. end enriched, double-strand cDNA was digested with Not I and cloned
19. into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library
19. was not normalized. Library was constructed by Life Technologies, a
19. division of Invitrogen.
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AL568796 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE005YL11
AL568796
                                                                                                                                                                                                                     284 CGTGTACCCCACTCAGCCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCCAA 343
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 904)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and Tadonato, S.P.

Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Biol. 6 (7), R60 (2005)
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Email: cmagness@illumigen.com
Sequenced on 2005.04.01. 592 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
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11.LINURIGEN MCQ 611545 Katze, MMOV Macaca mulatta cDNA clone
1181/UW:311396 57 similar to Bases 5 to 804 highly similar to human
COLIA1 (H8.172928), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
/dev_stage="adult"
/lab_host="Blectromax DH10B"
/clone lib="Katze_hMoV"
/note="Grgan: ovary; Vector: pDONR 222; Site 1: BsrG I;
Site 2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"
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2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
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BACKWARD: CACTAIAGGGCGAATTGGGTA
Insert Length: 904 Std Error: 0.00
Plate: CL000631 row: D column: 06
Seg primer: CCCTCACTAAAGGGAACAAAA
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1. .904
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/strain="Indian"
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PCR PRimers
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This sequence belongs to sequence cluster 8730.r

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                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Buteleostomi,
Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                 Smith, T. P. L., Freking, B. A., Ford, J. J., Vallet, J. L., Wise, T. A.,
Nonneman, D. J., Wray, J. B. and Keele, J. W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
Contact: Smith TPL
PO Box 166, Clay Center, NE 69933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Email: Smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pags sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified vcross match v0.990329.
Plate: TMW8073 row: P column: 20
Seq primer: GTAATACGACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 CGTGTACCCCACTCAGCCCCAGCGTGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCCCCCCTCAAGAGCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 CCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAGGCTGCAACCTGGACGCCATCAAAGTCTTCTGCAACATGGAGACAGGCGGGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIGITA CCCCACTCAGCCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 GGACAAGAGGCACGTCTGGTACGGCGAGAGCATGACCGACGGATTCCAGTTCGAGTACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 CGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /alone_lib="MARC 4PIG",
/note="Vector: pcDNA3.1; Site_1: BCORI; Site_2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                 S 867 bp mRNA linear MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 684; DB 8; 1
Pred. No. 2.2e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                 DN103076.1 GI:59775852
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.7%;
ilarity 94.7%;
Conservative
                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                       (bases 1 to 867)
                                                                                                                                               (pig)
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Matches 708; C
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                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                               JOURNAL
COMMENT
                 RESULT 5
DN103076
                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                            AUTHORS
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                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Taxon:9606"
/clone="Taxon:pdNSFONTA"
/note="vector: pcMVSFORT 6; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAA
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                                                                                                                                                                                                                                                                                                                                                      Gaps
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODEO05CF06NP1&c=8730.r. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                90.4%; Score 697; DB 1; Length 1035; 97.9%; Pred. No. 1.7e-156;
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                                                   1. .1035
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Matches 741; Conserv
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BP172484 BP172484 full-length enriched swine cDNA library, adult uterus Sus scrofa cDNA clone UTR010022F11 5', mRNA sequence.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                           1 (bases 1 to 820)
Cholshi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H. Okumura, N., Hamsima, N. and Awata, T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                    CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
                                                                                                                                                                                                                                                                             CETETACCCCCACTCAGCCCAGTGTGGCCCAGAACTGGTACATCAGCAAGAACCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 CACCGAGGCCTCCCAGAACATCACCTACCACGCAGAAACAGCGTGGCCTACGATGGACCA
                                         CCGTGACTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA
                                                                                                                                                                                               CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGGTGAAGACCTG
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                   CGTGTACCCCACTCAGCCCCAGTGTCGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
                                                                                                                                                                                                                                                                                                                        GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
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Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
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BP172484.1 GI:40421957
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                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 694)

1 and Endemberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
CACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCA
                                                                              CACTGAGGCTTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCA
                                                                                                                                  GCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCG
                                                                                                                                                                                                           CGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN342173 69934677 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence.
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Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 694 Std Brror: 0.00.
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/mol_type="mRNA"
/db_xrefe"taxon:9606"
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Contact: Brandenberger R
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CN342173.1 GI:47342107
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Best Local Similarity 99.4
Matches 683; Conservative
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                                                                                                                                                                                                                                                                                                   GSS 17-DEC-2003
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661 GATGTGGCCCCCTTGGACGTTGGCGCCCCGACGAGAATTCGGCATCGACCTTAGCCCT 720
                                                                                                                                                                                                                                                                          1378 bp DNA linear GSS 17-DEC-200 Pan troglodytes COL1Al gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 3378)

1 (bases 1 to 3378)

1 odd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriara, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Ban troglodytes
Eukaryots Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2640 TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCCCCCTCAAGAGCCTGAG
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Best Local Similarity 92.4%; Pred. No. 2.4e-152;
Matches 683; Conservative 0; Mismatches 56;
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Science 302 (5652), 1960-1963 (2003)
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/gene="COLIA1"
/locus_tag="HCM5321"
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                                                                                               741 GICTGCITCCIGIAAACICCCICC
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                                                                                     EMBAIL: huestishidestric.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute

Agrobiological Sciences and STAFF-Institute

Agrobiological Sciences and STAFF-Institute

Inbrary

Vector sequences were eliminated by RepeatMasker version 2002/07/13

and crossmatch version 0.990319

Low quality bases were trimmed based on the quality values.
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/mol_type="mRNA"
/db xref="texcn:9823"
/clone="uTRAD1022F11"
/tissue_type="uterus"
/fdev stage="adult"
/clone="lib="full-length enriched swine cDNA library, adult uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Indels
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 88.2%; Score 680; DB 3; 11 Similarity 94.6%; Pred. No. 2e-152; 704; Conservative 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                  1. .820
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/clone_lib="full-length enriched swine cDNA library, adult
uterus"
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CN342248
CN342548.1 GI:47342482
EST.
Homo sapiens (human)
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                                                                                                                                     874;
                                                                                                                                     Length
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                                                                                                                                Score 674.8; DB 3;
Pred. No. 3.5e-151;
0; Mismatches 42;
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                                                                                                                                    87.5%;
                                                                                                                                                   Best Local Similarity 94.3
Matches 700; Conservative
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Animal Genome Laboratory, Genome Research Department
Animal Genome Laboratory, Genome Research Department
Animal Genome Laboratory, Genome Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Email: 481-29-838-8627
Email: huenishi@affrc.go.jp
Ex; +81-29-838-8627
Email: huenishi@affrc.go.jp
EXT project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
Location/Qualifiers
                                           3119
                                                                                                                                                                                                                                                                                                              CGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACAC 3239
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uterus Sus
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae;
                                                                                     436
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                                                                                                                                                     CACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCA
                                                                                                                                                                        CACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCA
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                   GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
                                                                               CGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTC
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Jenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shink.

Okumura, N., Hamasima, N. and Awata, T.

PEDB (Pig EST Data Explorer): construction of a database for J
derived from porcine full-length cDNA libraries

Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP172845 full-length enriched swine cDNA linear EST BP172845 full-length enriched swine cDNA library, adult scrofe cDNA clone UTR010021G07 5', mENA sequence. BP172845 GI:40422318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGTCTGCTTCCTGTAA 3378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (pig)
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Eukaryota; N
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BP172845
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/ncce="Organ: Ovarian cortex; Vector: Lambda ZAP Express; Site_1: EcoR1; Site_2: Xhol; A bovine ovarian cortex cDNA library was constructed using the Lambda Zap Express/Gigapack cloning kit (Stratagene cloning systems). Express/Gigapack cloning kit (Stratagene cloning systems). CDNA synthesis was carried out using an oligo-(dT) primer for the reverse transcription of 5(g of mRNA and the library was constructed by directional cloning EcoR1-Xhol based on manufacturers instructions. An insert: vector ligation ratio of 1:5 was chosen as most optimum. The lambda library was packaged with Gigapack III gold packaging extracts and plated on the E. coli cell line XLI-Blue MRF'."
                                                                                                                                                                                                                                                                                                                                                                             CV547993 813 bp mRNA linear EST 03-JUN-2005 EST409 Bovine Lambda Zap Express ovarian cortex cDNA library Bos taurus cDNA clone ovca_001_b05 5' similar to Pro alpha 1 (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Ovarian cortex"
/dev_stage="Day 2, 6, 8 and 14 of the oestrus cycle"
/clone_lib="Bovine Lambda Zap Express ovarian cortex CDNA
library"
                    919
                                                              621
                                                                                                              919
                                                                                                                                                           681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotasi Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Beora; Bovidae; Bovidae; Bos.

1 (bases 1 to 613)
Casey,O.M., Fitzpatrick,R., McInerney,J., Powell,R. and Sreenan,J.M.

Sreenan,J.M.

Expressed Sequence Tag analysis of abundantly expressed bovine ovarian cortex genes
Unpublished (2004)
                                                  562 CGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGGGTCACAC
                                                                                                              617 CGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCAT
                                                                                                                                                           622 cogadoctrogogoaagacagroatroaaracaaaaccaccaagaccrocccar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ocasey@athenry.teagasc.ie
Insert Length: 813 Std Error: 0.00
Plate: ovarian cortex abundant plate 1 row: b column: 05
Seg primer: M13 reverse primer = caggaaacagctatgacc
High quality sequence stop: 813
POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Teagasc, Agriculture and Food Development Authority
Galway, Ireland
Tel: 00353 91 845845
Fax: 00353 91 845847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Casey OM
Animal Reproduction Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="ovca_001_b05"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                               677 CATCGATGTGGCCCCCTTG 695
                                                                                                                                                                                                                                      682 CATCGATGTGGCCCCCTTG 700
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AUTHORS
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CVS47993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tissue type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hBS cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCCAGGGCTCCCACCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTC 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTGACCTCAAGATGTGCCACTCTGAAGAGTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 201
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                                                                                                              Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, Li.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGACAAGAGGCCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
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                                                                                                                                                                                                                                                                                                          Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
741: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 700 Std Error: 0.00.
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Pred. No. 4.8e-151;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                        Contact: Brandenberger R
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                                                                   Hominidae, Homo.
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                      GAACATCCGGAGCCCCAAGAGCCGCAAGAACCCCGCCCCGCACCTGCCGTGACCTCAA 148
                                                                                                                                  328
                                                                                                                                                                                                                                 TCAGCCCCAGCGTGGCCCCAGAAGAACTGGTATATCAGCAAGAAACCCCAAGGAAAAAAGAGGGA 301
                                                                                                                                                                                                                                                                                CETCTGGTACGGCGAGAGCATGACCGGCGGATTCCAGTTCGAGTATGGCGGCCAGGGGTC 361
                                                                                                                                                                                                                                                                                                                               CGATCCTGCCGATGTGGCCCATCCAGCTGACTTTCCTGCGCCTGATGTCCACCGAGGCCTC 421
                                                                                                                                                                                                                                                                                                                                                                   508
                                                                                                                                                                                                                                                                                                                                                                                CCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAA 481
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Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H. Okumura,N., Hamasima,N. and Awata,T.
PRDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
                                                                                            GAACATCCGGAGCCCTGAAGGCAGCCGCAAGAACCCCGCCCCCCCTGCCGTGACCTCAA 121
                                                                                                                                                                   CCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCAC 268
                                                                                                                                                                                          ceredaridecarrangererrecancardeanacceereagaecerereraraccecae 241
                                                                                                                                                                                                                                                                                                                                                                                                                 CCTCAAGAAGGCCCTGCTCCTCAAGGCCTCCAACGAGATCGAGATCCGCGCCGAGGGCAA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721
                                             61
                                          GETCCETEACCETEACCTCGAGGTGGACACCACCTCAAGAGGCTGAGCCAGCAGAATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCAAGAAGGCCCTGCTCCTCCAGGGCTCCAACGAGATCGAGATCCGGGCCGAGGGCAA
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                                                                                                                                                                                                                                                                                                                  CGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTC
 Gaps
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 34;
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Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishidaaffrc.go.jp
Est project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/organism="Rus"
/db_xref="taxon:9823"
/cloine="type="tuterus"
/dev_stage="adult"
/dev_stage="adult"
/tensue_ltp="tuterus"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
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(1), D484-D488 (2004)
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Pred. No. 9.4e-151;
0; Mismatches 40;
Nucleic Acids Res. 32
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al Similarity 94.6%;
697; Conservative
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue type="embryonic stem cells, embryoid bodies
/tissue type="embryonic stem cells"
/tissue type="embryonic stem cells"
/clone lib="GRN EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
from embryoid body outgrowths derived from hES cell lines
from conditions."
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434
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(Lases 1 to 701)

Brandenberger,R., 2hang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                          298 TCCACCGAGCCTCCCCAGAACATCACCTACCACTGCAAGAACAGGGGGCCTACATGGAC
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375 GGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATG
                                        358 GGGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATG
                                                                                                                                                               CAGCAGACTCGACAACTCAAGAAGGCCCTGCTCCACAGGGCTCCAACGAGATCGAGATC
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                                                                                                                                                                                                                                                                                                                              615 ACCGGAGCCTGGGCAAGACAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCC
                                                                                435 TCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGAC
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17000532189205 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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230 Constitution Drive, Menlo Park, C
230 Constitution Drive, Menlo Park, C
Tel: 650 473 756
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 701 Std Brror: 0.00.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 796)
Fu.G.K., Mang.J.T., Yang.J., Au-Young.J. and Stuve, L.L.

Fu.G.K.: manglification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
                                                                                                        CCCCCTTGGACGTTGGCGCCCCTGACCAAGAATTCGGCATCGACCTTAGCCCTGTCTGCT
                         GCAAGACAGTGATCGAATACAAAACCACCAAGACCTCCCGCCTGCCCATCATCGATGTGG
                                                                                    CCCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u> AGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGGAAGCCGCAAGAACCCCGCCGCACC</u>
    GCAAGACAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGG
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CD607437
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/db_xref="taxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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Pred. No. 1.6e-150;
0; Mismatches 5;
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/organism="Homo sapiens"
                                                                                                                                                                 TCCTGTAAACTCCCTCC 764
                                                                                                                                                                                               TCCTGTAACTCCCTCC 737
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Homo sapiens
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Contact: Fu GK
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CD607437/c
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                                                                                                               1. .666
|/organism="Homo sapiens"
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|/lab host="DH10B TonA"
|/clone_lib="DFCI-vidal horfeome 1.1"
|/note="Grgan: mixed; Vector: pDONR223; Site_1: attB1.1;
|Site_2: attB2.1; Genome Res. 2004 Oct;14(10B):2128-35."
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBYI - vov; g column: 08
High quality sequence stop: 628.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Length 696;
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Pred. No. 2.8e-150;
0; Mismatches 11; Indels
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Best Local Similarity 98.4%;
Matches 677; Conservative C
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AGENCOURT_51294715 DRCI-Vidal horfeome 1.1 Homo sapiens cDNA clone IMAGE:40029743 3', mRNA sequence.
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                                                                                                                   CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 196
                                                                                                                                       CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG 265
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                              TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAG
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1 (bases 1 to 696)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MG(Mupublished (1999))

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Marc Vida

Tissue Procurement: Marc Vida
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Sequence 22, Appl Sequence 215, Appl Sequence 215, App Sequence 215, App Sequence 215, App Sequence 215, App Sequence 214, App Sequence 257, App Sequence 25
                                                                                                                                 April 27, 2006, 18:34:23; Search time 161.848 Seconds (without alignments) 8467.835 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 257,
Sequence 192,
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/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/R_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-09-404-879A-257
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APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY (
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY (
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/318,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SEQ ID NOS: 312
LENGTH: 590
LENGTH: 590
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; Patent No. 6488931
; GENERAL INFORMATION:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(590)
OTHER INFORMATION: n = A,T,C or G
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US-09-338-933-215
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; Betent No. 6468546
; GENERAL INFORMATION:
APPLICANT: Mitchan, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REPERENCE: 210121.462C2
; CURRENT FILING DAGE: 1999-09-24
; CURRENT FILING DAGE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SEQ ID NOS: 393
; SEQ ID NOS: 393
; SEQ ID NO 215
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) LOCATION: (1)...(590)

) OTHER INFORMATION: n = A,T,C or

US-09-404-879A-215
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ORGANISM: Homo sapien
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US-09-404-879A-215
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Petent No. 6670463
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon B.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT PELICATION NUMBER: US/09/216,003A
CURRENT PILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGGAGAGTACTGGATTGACCCCAA 359
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Pred. No. 3.3e-83;
0; Mismatches 6; Indels 0
                  Sequence 215, Application US/09215681A
Fatent No. 6528253
Fatent No. 6
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; LOCATION: (1)...(590)
; OTHER INFORMATION: n = A,T,C or G
US-09-215-681-215
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Best Local Similarity 98.5%;
Matches 394; Conservative
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ORGANISM: Homo sapien
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US-09-216-003A-215
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Oarter, Darrick
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
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98.5%; Pred. No. 3.3e-83;
tive 0; Mismatches 6
FEATURE:
NAME/KEY: modified_base
LOCATION: (8)
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LOCATION: (9)
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US-09-216-003A-215
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LOCATION: (1)...(590)
OTHER INFORMATION: n = A,T,C or
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; Sequence 215, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
   APPLICANT: Retref. Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.46266
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT PILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SEQ ID NO 215
; LENGTH: 590
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98.5%; Pred. No. 3.3e-83;
tive 0; Mismatches 6;
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Best Local Similarity 98.5
Matches 394; Conservative
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ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGTACCCCACTCAGCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACAAGAGGCATGTCTGGTTCGGCGAGGATGACCGATGGATTCCAGTTCGAGTATGG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG 539
                                                                                                                                                                                                                                                                                                      CCGTGACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 196
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                                                                                                                                                       CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
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; Sequence 215, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Ranger, Gary R.
; APPLICANT: Hill, Panger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: 105/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
                                              Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 390.4; DB 3; Length 9 Pred. No. 3.3e-83; 0; Mismatches 6; Indels
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCCAGGGCTCCCACCCTGCCGATGTGGACCTCCGGCCG 579
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                                        Score 390.4; DB 3;
Pred. No. 3.3e-83;
0; Mismatches 6;
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                                          Query Match 50.6%;
Best Local Similarity 98.5%;
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.5%;
Matches 394; Conservative
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LOCATION: 8, 9
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ORGANISM: Homo sapiens
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US-10-198-053-215
    US-09-667-857-215
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229 CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAACCTG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 594;
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APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
APPLICANT: Fring, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
TITLE OF INVENTION: OP OVARIAN CANCER
TITLE OF INVENTION: 0P OVARIAN CANCER
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FABLESQ for Windows Version 3.0
SEQ ID NO 214
LENGTH: 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.5%; Score 389.2; DB 3; 99.2%; Pred. No. 6.3e-83; tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SEQ ID NO 214
LENGTH: 594
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                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: misc feature
LOCATION: (1)...(594)

OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc feature
LOCATION: (1)...(594)
CTHER INFORMATION: n =
US-09-215-681-214
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity
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ORGANISM: Homo sapien
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US-09-215-681-214/c
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; Sequence 214, Application US/09404879A
; Sequence 214, Application US/09404879A
; Detent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Middler, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; CURRENT APPLICATION NUMBER: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 214
LENGTH: 594
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Sequence 214. Application US/09338933

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
                                              540 CGGCCAGGGCTCCCACCCTGCCGATGTGGACCTCCGGCCG 579
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; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-214
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Matches 391; Conservative
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NAME/KEY: misc feature
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137 CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 196
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                        137 CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGTACTGGATTGACCCCAA 196
                                                  289 CCGTGACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 230
                                                                                                                                             229 CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG 170
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US-09-667-857-214/C

i Sequence 214, Application US/09667857

j Patent No. 6699664

i GENERAL INFORMATION:
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Ring, Gordon E.
    APPLICANT: Ring, Steven P.
    APPLICANT: Retter, Marc W.
    APPLICANT: Retter, Marc W.
    APPLICANT: Retter, Marc W.
    APPLICANT: Retter, Marc W.
    APPLICANT: Retter, Darrie, Steven G.
    APPLICANT: Red, Steven G.
    APPLICANT: Red, Steven G.
    APPLICANT: Red, Steven G.
    APPLICANT: Nedvick, Thomas S.
    APPLICANT: Carter, Darriek,
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
    TITLE OF INVENTION: DAGNOSIS OF OVARIAN CANCER
    FILE REFERENCE: 210121.462C5
    CURRENT APPLICATION NUMBER: US/09/667,857
    CURRENT PILING DATE: 2000-09-20
    NUMBER OF SEQ ID NOS: 455
    SOFTWARE: FRAESEQ for Windows Version 3.0
    SEQ ID NO 214
    LENDER FOR THE THERAPY AND SEQ ID NOS: 455
    SOFTWARE: REALSEQ for Windows Version 3.0
    SEQ ID NO 214
    LENDER FOR THE THERAPY AND SEQ ID NOS: 455
    SOFTWARE: REALSEQ for Windows Version 3.0
    SEQ ID NO 214
    LENDER FOR THE THERAPY AND SEQ ID NOS: 455
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99.2%; Pred. No. 6.3e-83;
tive 0; Mismatches 3;
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NAME/KEY: misc_feature
LOCATION: (1)...(594)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 99.2
Matches 391; Conservative
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ORGANISM: Homo sapien
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APPLICANT: Mitchen, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 214
LENGTH: 594
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Pred. No. 6.3e-83;
0; Mismatches 3; Indels
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COTHER INFORMATION: Where n is a, c, g or t
US-09-216-003A-214
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US-09-216-003A-214/c
Sequence 214, Application US/09216003A
Patent No. 6670463
GENERAL INFORMATION:
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OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
LOCATION: (585)
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OTHER INFORMATION: Where n is
NAME/KEY: modified_base
  Best Local Similarity 99.2
Matches 391; Conservative
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Matches 391; Conservative
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; Sequence 214, Application US/10198053
; Patent No. 685710
; GENERAL INFORMATION:
    APPLICANT: Bangur, Chaitanya S.
    APPLICANT: Retter, Marc W.
    APPLICANT: Fanger, Gary R.
    APPLICANT: Fanger, Gary R.
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
    TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
    TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
    TITLE OF INVENTION: UND 1146209
    CURRENT APPLICATION NUMBER: US/10/198,053
    CURRENT FILING DATE: 2002-07-17
    NUMBER OF SEQ ID NOS: 624
    SOFTWARE: PastSEQ for Windows Version 4.0
    SEQ ID NO 214
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                                                                                                                            CGGCCAGGGCTCCGACCCTGCCGATGTGGCCATC 410
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OTHER INFORMATION: n = A,T,C or G
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US-10-198-053-214/c
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Sequence 114, Application US/09827271
| Patent No. 6562980
| GENERAL INFORMATION:
| APPLICANT: Reter, Marc W. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE |
| TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER |
| TITLE REFERENCE: 210121.462C6 |
| CURRENT APPLICATION NUMBER: 0S/09/827,271 |
| CURRENT PILLING DATE: 2001-04-04 |
| NUMBER OF SEQ ID NOS: 461 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LENGTH: 594 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.5%; Score 389.2; DB 3; Best Local Similarity 99.2%; Pred. No. 6.3e-83; Matches 391; Conservative 0; Mismatches 3;
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Job time : 163.848 secs
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// LOCATION: (1)...(594)

// OTHER INFORMATION: n = A,T,C or

US-09-827-271-214
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136, App
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                                                                                                                                                                                                                                      (without alignments)
9144.835 Million cell updates/sec
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                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-78-12-18

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Sequence 3, Application US/10677877A

Faguence 3, Application US/1067787A

Fublication No. US20050202537A1

GENERAL INFORMATION:

APPLICANT: Liang, Pency GenHunter Corporation

TITLE OF INVENTION: Methods and composition for producing secreted trimeric

TITLE OF INVENTION: receptor analogs and biologically active fusion proteins

TITLE OF INVENTION: US-PL

CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 3

LENGTH: 771
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US-10-177-293-64

US-10-310-822-3-64

US-10-843-6418-521

US-10-843-6418-521

US-10-843-6418-3809

US-10-852-335A-63

US-10-979-159-260

US-10-291-265-7

US-10-291-265-7

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Matches 771; Conservative
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LOCATION: (12)...(755)
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Sequence 7, Application US/10677877A

Sequence 7, Application US/10677877A

Publication No. US20050202537A1

GENERAL INFORMATION:
APPLICANT: Liang, Peng, GenHunter Corporation
APPLICANT: Liang, Peng, GenHunter Corporation
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 7
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1848 CCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGAC 1907
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                       1428 ACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAAC
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ORGANISM: Homo sapiens
FEATURE:
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TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 15
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US-10-677-877A-15
Sequence 15, Application US/10677877A
; Publication No. US2005022537A1
; GENERAL INFORMATION:
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; NAME/KEY: CDS
; LOCATION: (24)...(1931)
US-10-677-877A.15
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Best Local Similarity
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Sequence 1, Application US/10677877A

Publication No. US2005020537A1

Publication No. US2005020537A1

APPLICANT: Liang, Peng; GenHunter Corporation

TITLE OF INVENTION: Methods and composition for producing secreted trimeric

TITLE OF INVENTION: Teceptor analogs and biologically active fusion proteins

TITLE REPERENCE: 03-05-PL

CURRENT APPLICATION NUMBER: US/10/677,877A

WUMBER OF SEQ ID NOS: 16

SEQ ID NO 1

LENGTH: 963
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CCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGA
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Best Local Similarity 100.0
Matches 755; Conservative
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ORGANISM: Homo sapiens
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US-10-677-877A-1
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TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL
CURRENT APPLICATION NUMBER: US/10/677,877A
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 11
                                    CCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAAGACTGGTGAG 1774
                                                                                                                  1775 ACCTGCGTGTACCCCACTCAGCCCAGTGGGCCCCAGAAGAACTGGTACATCAGCAAGAAC 1834
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Best Local Similarity 100.0%; Pred. No. 3.4e-211;
Matches 759; Conservative 0; Mismatches 0;
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; Sequence 11, Application US/10677877A
; Publication No. US20050202537A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-677-877A-11
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US-10-677-877A-13
Query Match
Best Local S:
Matches 755
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Subjunction No. US20050202537A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Methods and composition for producing secreted trimeric

TITLE OF INVENTION: receptor analogs and biologically active fusion proteins

FILE REFERENCE: 03-052-PL

CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 9
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CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
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                                    CCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAAGAACCCCGCCGCACCTG
                                                                                                    CCGTGACTCAAGATGTGCCACTCTGACTGGAAGAGTGGGAGGTACTGGATTGACTGAA
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ORGANISM: Homo s
FEATURE:
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; LOCATION: (18)
US-10-677-877A-9
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US-10-677-877A-9
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Sequence 13, Application US/10677877A

Publication No. US200502537A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Liang, Pengi GenHunter Corporation

TITLE OF INVENTION: Receptor analogs and biologically active fusion proteins

TITLE OF INVENTION: receptor analogs and biologically active fusion proteins

TITLE OF INVENTION: 10022-101

CURRENT APPLICATION NUMBER: 108/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 13

LENGTH: 2139
                                                                                                           1460 GCAGACTGGCAAGAAGGCCCTGCTCCTCAAGGCTCCAACGAGATCGAGATCG 1519
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    Length 1734;
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ch 97.9%; Score 755; DB 9; Le 11 Similarity 100.0%; Pred. No. 5.1e-210; 755; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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; Sequence 66, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
 16
                                                     FEATURE:

NAME/KEY: CDS

LOCATION: (12)...(2471)

US-10-677-877A-5
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 SEQ ID NOS:
                               TYPE: DNA
ORGANISM: Homo
NUMBER OF SEQ 1
SEQ ID NO 5
LENGTH: 2487
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US-10-177-293-66
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Publication No. US20050202537A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
TITLE OF UNENTION NUMBER: US/10/677,877A
CURRENT APPLICATION NUMBER: US/10/677,877A
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100.0%; Pred. No. 5.4
ive 0; Mismatches
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                    ; LOCATION: (24)...(2123)
US-10-677-877A-13
                                                                 Similarity
          NAME/KEY: CDS
LOCATION: (24
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Best Local S
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                                                   Gaps
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  Length 2487;
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Query Match 97.9%; Score 755; DB 9; L. Best Local Similarity 100.0%; Pred. No. 5.5e-210; Matches 755; Conservative 0; Mismatches 0;
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Annahan, John E.
APPLICANT: Hibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: THIBODE TOWER GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029PZRNM
CURRENT APPLICATION NUMBER: US 60/361,978
FRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LEADER APPLICATION NUMBER: US 60/361,988
MANDER FRIENCE FASTSEQ for Windows Version 4.0
SEQ ID NO 29
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                                                                                                                                                                                 1256 gcagacticscaacctcaagaaggcccriscriccaagggcriccaacgagarcgagarccg
                                                                                                                                                                                                                                                     557 CGCCGAGGCCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACAC
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Best Local Similarity 100.0%; Pred. No. 9.9e-209;
Matches 751; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               737 CCCTGTCTGCTTCCTGTAACTCCCTCCATC 767
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APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/10301822
Publication No. US20030148410A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berger, Allison
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; LOCATION: (120)...(4514)
US-10-301-822-29
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ORGANISM: Homo Sapiens
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APPLICANT: Wangy Youzhen
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APPLICANT: Wangy Youzhen
APPLICANT: Woerech, Sebastian
APPLICANT: Montahan, John
APPLICANT: Montahan, John
APPLICANT: Montahan, John
APPLICANT: Metch.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Metch.
APPLICANT: Metch.
APPLICANT: Metch.
APPLICANT: Sahin, Ayesgul
APPLICANT: Sahin, Ayesgul
APPLICANT: Sahin, Ayesgul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE REPERENCE: Mr. 08 60/299, 887
TITLE OF INVENTION WUMBER: US 60/309, 887
PRIOR FILING DATE: 2001-06-21
PRIOR PLILOR OF SOURCES: SOURCES: US 60/305, 501
PRIOR PLILOR OF SOURCES: US 60/305, 501
PRIOR PLILOR OF SOURCES: US 60/305, 502
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-05-05
PRIOR FILING DATE: 20
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Zhao, Xumei
Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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CORGANISM: Homo sapiens
US-10-177-293-66
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               3776 TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCCCCCAAGAGCCTGAG
                                                                          CGGTGACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA
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TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAG
                                                           GCAGACTGGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCAACGAGATCGAGATCCG
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; Sequence 12, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INPORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using
; FILE REFERENCE: 1657/2012
; CURRENT PELLING DATE: 2007-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
INNETH: 5921
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CORGANISM: Homo sapiens
US-10-734-564-12
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Best Local Similarity
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                                 3896 CCGTGACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA 3955
                                                                                           3956 CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG 4015
                                                                                                                                                  4136 CGGCCAGGGCTCCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTC 4195
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                                                                        CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG 256
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                                                                                                                                    CGTGTACCCCACTCAGCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA 316
                                                                                                                                                                                                                                                            CGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTC 436
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               CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA
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100.0%; Pred. No. 9.9e-209;
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WS-10.74.
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WS-10.74.
Sequence 18, Application US/10764425
; Publication No. US20040146921A1
; GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Taylor, Deepa
APPLICANT: Taylor, Ian
APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLO;
FILE REFERENCE: 5151
CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT APPLICATION NUMBER: 60/442,582
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SGCTWARE: PatentIn version 3.2
; LENGTH: 5921
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Best Local Similarity 100.
Matches 751; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-788-792-23
US-10-788-792-23

Sequence 23, Application US/10788792

Publication No. US20040191819A1

GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Bigwood, Douglas
FILE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
FILE REFRENCE: 5152
CURRENT TILING DATE: 2004-02-27

FRICH APPLICATION NUMBER: US 60/450,655
PRIOR PLING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 254

SEQ ID NO 23
LENGTH: 5921
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                        TGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCACCAAGAGCCTGAG
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Sequence 2288, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
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Query Match 97.4%; Score 751; DB 8; Le Best Local Similarity 100.0%; Pred. No. 9.9e-209; Matches 751; Conservative 0; Mismatches 0;
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                                                                                                         Length 5921;
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100.0%; Pred. No. 9.9e-209;
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CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION WUMBER: 60/429,739
PRIOR FILING DATE: 200-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 2288
LENGTH: 5921
                                                                                                                          Matches 751; Conservative
                                                                               sapiens
                                                                                                                  Similarity
                                                                   TYPE: DNA
CRGANISM: Homo
US-10-723-860-2288
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APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OP INVENTION: NUCLBIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OP INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 340
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CRGANISM: Homo sapiens
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Search

RESULT 15
US-10-956-157-340
Sequence 340, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:

Job time : 699.19 secs

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April 27, 2006, 18:58:56; Search time 530.452 Seconds (without alignments) 5902.968 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 29, Appl	Sequence 138, App	Sequence 27, Appl	~	Sequence 244, App	Sequence 7, Appli	Sequence 479, App		Sequence 106, App		Sequence 1017, Ap	Sequence 1195, Ap	Sequence 991, App	Sequence 81, Appl	Sequence 215, App	Sequence 826, App	Sequence 869, App	Comission 946 Ann
SUMMARIES	ID	US-11-186-284-29	US-10-501-035-138	US-11-186-284-27	US-11-021-603-1	US-10-821-234-244	US-11-000-463-7	US-11-000-463-479	US-11-091-883-105	US-11-091-883-106	US-10-784-004-583	US-10-784-004-1017	US-10-784-004-1195	US-11-108-172-991	US-10-784-004-81	US-10-784-004-215	US-10-784-004-826	US-10-784-004-869	110-11-100-177-966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 27, Application US/11186284; Publication No. US20050266493A1; GENERAL INFORMATION:
                                                    Query Match 97.4
Best Local Similarity 100.
Matches 751; Conservative
ORGANISM: Homo sapiens
     , US-10-501-035-138
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Sequence 138, Application No. US20060046249A1

Publication No. US20060046249A1

GENERAL INPORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE

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Best Local Similarity 100.0%; Pred. No. 5.6e-191;
Matches 751; Conservative 0; Mismatches 0;
                                                                                                                                                                                         US-11-021-603-1

Sequence 1, Application US/11021603

Publication No. US20060003954A1

GENERAL INFORMATION:

APPLICANT: Beri, Rajinder

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES

FILE REFERENCE: 06275-254US1

CURRENT APPLICATION NUMBER: US/11/021,603

FRIOR PRIOR APPLICATION NUMBER: US/10/149,352

PRIOR FILING DATE: 2004-12-21

PRIOR APPLICATION NUMBER: PCT/GB00/04741

PRIOR APPLICATION NUMBER: GB 9929487.8

PRIOR APPLICATION NUMBER: GB 9929487.8

PRIOR RILING DATE: 1999-12-15

NUMBER: OF SEQ ID NOS: 14

SOFTWARE: PATENTING DATE: 1999-12-15

NUMBER: OF SEQ ID NOS: 14
                                                                                                            CCTGTCTGCTTCCTGTAAACTCCCTCCATC 4526
                                                                                       CCCTGTCTGCTTCCTGTAAACTCCCTCCATC 767
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ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (120)..(4511)
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NAME/KEY: sig_peptide

LOCATION: (120)..(185)

US-11-021-603-1
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TITLE OF INVENTION: MCTL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THIRD OF INVENTION: THE PROPERTY OF COLON CANCER
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR PILING DATE: 2005-07-21
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR PILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR PILING DATE: 2002-05-05
SUGTWARE PILING DATE: 2002-05-05
SUGTWARE PRIOR APPLICATION NUMBER: US 60/381,988
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; NAME/KEY: CDS
; LOCATION: (120)...(4514)
US-11-186-284-27
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ORGANISM: Homo Sapiens
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                                                                                                                 437 CACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCA
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1 Sequence 7, Application US/11000463
1 Publication No. US20050266423A1
2 GENERAL INFORMATION:
1 APPLICANT: Tang, Y Tom
3 APPLICANT: Asundi, Vinod
4 APPLICANT: Asundi, Vinod
5 APPLICANT: Asundi, Vinod
5 APPLICANT: Chen Rui-hong B.
5 APPLICANT: Chen Rui-hong B.
5 APPLICANT: Asundi, Vinod
5 APPLICANT: Chen, Rui-hong B.
5 APPLICANT: Chen, Pined
6 APPLICANT: Chen, Pined
6 APPLICANT: Cheng
7 APPLICANT: Cheng
7 APPLICANT: Drmanac, Radoje T.
7 TITLE OF INVERTION: Novel Nucleic Acids and Polypeptides
6 APPLICANT: Drmanac, Radoje T.
7 TITLE OF INVERTION: Novel Nucleic Acids and Polypeptides
7 TITLE OF INVERTION: NUMBER: 10/291,265
7 PRIOR APPLICATION NUMBER: 09/922,279
7 PRIOR APPLICATION NUMBER: 09/921,404
7 PRIOR APPLICATION NUMBER: 09/491,404
7 PRIOR APPLICATION NUMBER: 09/431,451
7 PRIOR APPLICATION NUMBER: 09/631,451
7 PRIOR PILING DATE: 2000-09-15
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LOCATION: (140)..(4531)
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                                                                                                                                                                                       1316 CGCCGAGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACAC 4375
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ IN NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 244
LENGTH: 4749
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                                                                                                                                                                                                                                                                     4376 CGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCAT
                                             497 GCAGACTGGCAACCTCAAGAAGGCCCTGCTCCAAGGGCTCCAACGAGATCGAGAGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGTCTGCTTCCTGTAAACTCCCTCCATC 4526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 748; Conserva
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US-10-821-234-244
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## APPLICANT: Cao, Yi-Cheng
### APPLICANT: Drmanac, Radoje T.
### TITLE OF INVENTION: Novel Mucleic Acids and Polypeptides
### FILE REPERENCE: 785CIP4CN
### CURRENT FILING DATE: 2004-11-29
### CURRENT FILING DATE: 2004-11-29
### PRIOR APPLICATION NUMBER: UC/291,265
### PRIOR APPLICATION NUMBER: PCT/US01/02623
### PRIOR APPLICATION NUMBER: 09/922,279
### RIOR PLILING DATE: 2001-03-25
### PRIOR PLILING DATE: 2001-03-25
### PRIOR PLILING DATE: 2001-03-25
### PRIOR PLILING DATE: 2000-01-25
### PRIOR PLILING DATE: 2000-01-25
### PRIOR PLILING DATE: 2000-01-25
### PRIOR PLILING DATE: 2000-01-17
### PRIOR PLILING DATE: 2000-01-17
### PRIOR PLILING DATE: 2000-09-15
### PRIOR PRILING DATE: 2000-09-15
### PRIOR PRINCE DAT
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| LOCATION: (1)...(4791)
| OTHER INFORMATION: n = a,t,c or
US-11-000-463-479
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                                                                                                               Gaps
                                                          Score 746.2; DB 14; Length 4770;
Pred. No. 1e-189;
0; Mismatches 3; Indels 0;
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APPLICANT: Tang, Y Tom
APPLICANT: Abundi, Vinod; APPLICANT: Chen, Rui-hong; APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
                                                            96.8%;
                                                       Query Match 96.8
Best Local Similarity 99.6
Matches 748; Conservative
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2966 TGATGCCAATGTGGTTCGTGACCTGGACCTCGAGGTGGACACCCTCAAGAGCCTGAG 2907
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LOCATION: (1542)..(1545)
OTHER INFORMATION: a, c, g,
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LOCATION: (2871)...(2871)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (2873)..(2873)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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NAWE/KEY: modified base
LOCATION: (1692)...(1692)
FEATURE:
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LOCATION: (1420)...(1424)
OTHER INFORMATION: a, c,
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LOCATION: (1931)...(1938)
OTHER INFORMATION: a, c,
                                                          FEATURE: modified base LOCATION: (1207)..(1207) OTHER INFORMATION: a, c,
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LOCATION: (1892)...(1892)
OTHER INFORMATION: a, c,
                      LOCATION: (1203).. (1203)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                              LOCATION: (1485)..(1485)
OTHER INFORMATION: a, c,
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LOCATION: (1501)..(1501)
OTHER INFORMATION: a, c,
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OTHER INFORMATION: a, c,
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LOCATION: (1940)..(1948)
OTHER INFORMATION: a, c,
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LOCATION: (2009)...(2009)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
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                                                                                                                                                                                                                                                                                                                                               Sequence 105, Application US/11091883
| Sequence 105, Application US/11091883
| Publication No. US20060024693A1
| GENERAL INFORMATION:
| APPLICANT: CIBELL, JOSE
| APPLICANT: CIRCLANT: CROSBAS, ARIFF
| APPLICANT: CROSBAS, ARIFF
| APPLICANT: CROSBAS, ANTER A. TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN TITLE OF INVENTION: UNBILITY
| TITLE OF INVENTION: UNBER: US/11/091,883
| CURRENT FILING DATE: 2004-03-29
| FILE REPRENCE: 5394JUS
| CURRENT FILING DATE: 2004-03-29
| NUMBER OF SEQ ID NOS: 513
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 105
| LENGTH: 6741
4476 CATCGATGTGGCCCCCTTGGACGTTGGTGCTCCCAGACTAGGAATTCGGCTTCGACGTTGG 4535
                                                                                                                                           CATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGG 736
                                                                                                                                                                                                                                                 4536 CCCTGTCTGCTTCCTGTAAACTCCCTCCATC 4566
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NAME/KEY: modified base
LOCATION: (760)..(760)
OTHER INFORMATION: a, c, g, or t
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NAME/KEY: modified base
LOCATION: (762)..(766)
OTHER INFORMATION: a, c, g, or t
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LOCATION: (810)..(810)
OTHER INFORMATION: a, c, g, or
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LOCATION: (768)..(775)
OTHER INFORMATION: a, c, g,
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LOCATION: (777)..(782)
OTHER INFORMATION: a, c, g,
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LOCATION: (812)..(812)
OTHER INFORMATION: a, c, g,
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LOCATION: (758)..(758)
OTHER INFORMATION: a, c,
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ORGANISM: Homo sapiens
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US-11-091-883-105/c
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FEATURE:
NAME/KEY: modified base
LOCATION: (1931)...[1938)
OTHER INFORWATION: a, c, g, or t
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NAME/KEY: modified base
LOCATION: (928)..(928)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (777)..(782)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (810)..(810)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified base
LOCATION: (1420)..(1424)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
FEATURE:
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OTHER INFORMATION: a, c, g,
FEATURE:
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LOCATION: (1841)...[1841)
OTHER INFORMATION: a, c, g,
                                                                                  NAME/KEY: modified base
LOCATION: (760)..(760)
OTHER INFORMATION: a, c, g,
FEATURE:
LOCATION: (762)..(766)
OTHER INFORMATION: a, c, g,
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LOCATION: (1542).. (1545)
OTHER INFORMATION: a, c, g
FRATURE:
NAME/KEY: modified base
                NAME/KEY: modified base
LOCATION: (758)..(758)
OTHER INFORMATION: a, c,
FEATURE:
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LOCATION: (812)..(812)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
LOCATION: (1203)..(1203)
OTHER INFORMATION: a, c,
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LOCATION: (1207)...(1207)
OTHER INFORMATION: a, c,
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NAME/KEY: modified base
LOCATION: (1892)...(1892)
OTHER INFORMATION: a, c,
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LOCATION: (1501)..(1501)
OTHER INFORMATION: a, c,
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US-11-091-883-106/c
; Sequence 106, Application US/11091883
; Publication No. US2006024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: CIBELLI, JOSE
; APPLICANT: CIBELLI, JOSE
; APPLICANT: CORDAS, ARIF
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CORSEN, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; TITLE OF INVENTION: VIABILITY
; FILE REPERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT APPLICATION NUMBER: 60/556,875
; PRIOR PELING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SEQ ID NO 106
; LENGTH: 6741
; TENGTH: 6741
CATOGATGTGGCCCCCTTGGACGTTGCCCCCAGACACTTCGGCTTCGACGTTGG 2247
                                                                                          2846 CCGTGACCTCCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCCAA 2787
                                                                                                                                                              2786 CCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG 2727
                                                                                                                                                                                                                                2726 CGTGTACCCCACTCAGCCCAGTGGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCCAA 2667
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                                                                                                                                                                                                               257 CGTGTACCCCACTCAGCCCCAGTGTGGCCCCAGAAGAACTGGTACATCAGCAAGAACCCCAA 316
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                                                                     137 CCGTGACCTCAAGATGTGCCCACTCTGACTGGAAGAGTGGAGGAGTACTGGATTGACCCCAA 196
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ORGANISM: Homo sapiens
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                   2306 CATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGG
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677 CATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGG
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Best Local Similarity 99.3%; Pred. No. 7.3e-189;
Matches 746; Conservative 0; Mismatches 5;
                                                                                                                                                                                    Sequence 583, Application US/10784004
Fublication No. US20060084066A1
GENERAL INFORMATION:
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REPERENCE: 08201.6029-00000
CURRENT APPLICATION UNMER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
                                                                                      2246 CCCGGTCTGCTGTAAACTCCCTCCATC 2216
                                                                  737 CCCTGTCTGCTTCCTGTAAACTCCCTCCATC 767
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: human
                                                                                                                                                       RESULT 10
US-10-784-004-583
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LOCATION: (3380)..(3380)
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              LCCATION: (1940)...(1948)
OTHER INFORMATION: a, c, g, o)
FEATURE:
CCATION: (2009)...(7009)
OTHER INFORMATION: a, c, g, o)
FEATURE:
NAME/KEY: modified base
LCCATION: (2871)...(2871)
OTHER INFORMATION: a, c, g, o)
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LOCATION: (2873)...(2873)
OTHER INFORMATION: a, c, g,
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Matches 747; Conservative
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NAME/KEY: modified base
LOCATION: (3020)..(3020)
OTHER INFORMATION: a, c,
 NAME/KEY: modified base
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96.4%; Score 743; DB 7; L
Best Local Similarity 99.3%; Pred. No. 7.3e-189;
Matches 746; Conservative 0; Mismatches 5;
                                                                                                                                                                                                      Sequence 1155, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION:
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SEQ ID NO 1195
; LENGTH: 4752
                                                                                                                          ; TYPE: DNA
; ORGANISM: human
US-10-784-004-1195
                                                                                                                                                                               RESULT 12
US-10-784-004-1195
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99.3%; Pred. No. 7.3e-189;
tive 0; Mismatches 5;
                                                                                                                                                                        Sequence 1017, Application US/10784004

Publication No. US20060084066A1

GENERAL INFORMATION:

APPLICANT: Biogen Idec

TITLE OF INVENTION: Surrogate Markers of Pain

FILE REPERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SEQ ID NO 1017

LENGTH: 4752
                                                                              Query Match 96.4 Best Local Similarity 99.3 Matches 746; Conservative
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: human
US-10-784-004-1017
                                                                                                                                                     RESULT 11
US-10-784-004-1017
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Sequence 81, Application US/10784004
Publication No. US20660084066A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SEQ ID NO 81
LENGTH: 5721
TYPE: DNA
ORGANISM: rat
US-10-784-004-81
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APPLICANT: Skeiky, Yagir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108.172
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-04-15
PRIOR APPLICATION NUMBER: US 09/649, 811
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-03-16
PRIOR PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR PRIOR FILING DATE: 2000-03-16
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PRIOR FILING DATE: 2000-03-16
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Pred. No. 3.1e-165;
0; Mismatches 3;
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APPLICANT: Lodes, Michael J.
APPLICANT: Secriet, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Reagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Ring, Gordon E.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
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Best Local Similarity 99.5
Matches 656; Conservative
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; ORGANISM: Homo sapiens
US-11-108-172-991
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                          CCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAA
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Fublication No. US20060084066A1
GENERAL INFORMATION:
APPLICANT: Biogen Idec
TITLE OF INVENTION:
FILE REFERENCE: 08201.6029-00000
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SEQ ID NO 215
LENGTH: 5721
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Matches 682; Conservative
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US-10-784-004-215
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US-10-784-004-215
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Aea28571 Human col	Aea28583 Human sol	Aea28575 Human alk	Aea28579 Human sol	Aea28569 Human col	Aea28577 Human sol	Aea28581 Human sol	Aea28573 Human alk	Ads98184 Protein f	Aab82454 Human pro		Abp68610 Human pan	Abu54471 Human tum	Abr47417 Breast ca	Abr92064 Human cer	Add14142 Human src	Adp65246 Human alp	Adq19470 Human sof	_	Adv87000 Collagen	Adv70233 Tumor-ass	Adz26573 Human typ	Adz09874 Human bre	Aea04480 Human pro
SUMMARIES	αı	AEA28571	AEA28583	AEA28575	AEA28579	ARA28569	AEA28577	AEA28581	AEA28573	ADS98184	AAB82454	ABB90764	ABP68610	ABUS4471	ABR47417	ABR92064	ADD14142	ADP65246	ADQ19470	ADQ29653	ADV87000	ADV70233	ADZ26573	ADZ09874	AEA04480
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Aae38634 Human col	Aaw12845 Pro-alpha	Aay56800 Human pre	Abg93947 Human pol	Humar	Add45059 Human Pro	Add45055 Human Pro	Add45051 Human Pro	Adr16800 Human col	Adr16425 Human col	Adr99144 Collagen,	Amino	Add26744 Human adi	Abr41631 Human DIT	Aab43439 Human can	Ade87049 Human pan	Ade87052 Human pan	Ade87050 Human pan	Aau14136 Human nov	Ade87048 Human pan	Ade87051 Human pan
7 AAE38634	2 AAW12845	3 AAY56800	5 ABG93947	2 AAW68485	7 ADD45059	7 ADD45055	7 ADD45051	8 ADR16800	B ADR16425	B ADR99144	9 ADX58061	7 ADD26744	5 ABR41631	3 AAB43439	7 ADE87049	7 ADE87052	7 ADE87050	4 AAU14136	7 ADE87048	7 ADE87051
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25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be protein secretion; fusion protein; protein activation; collagen I. Human collagen alpha(I) C-propeptide T2 construct protein. AEA28571 standard; protein; 247 AA. 04-OCT-2004; 2004WO-US032753. 02-OCT-2003; 2003US-00677877. (first entry) (GENH-) GENHUNTER CORP. WPI; 2005-386406/39. N-PSDB; AEA28570. WO2005047850-A2. sapiens. *>* 28-JUL-2005 26-MAY-2005. Synthetic. trimerized AEA28571; Liang P; Ношо **AEA2857** 

Claim 14; SEQ ID NO 4; 47pp; English

The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an inferame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide capable of self-trimerization which is heterologous to the first polypeptide to be trimerized, and introducing the construct into a eukaryotic cell. Receptor dade-oys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease

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treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ilgand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their maturally occurring trimeric ligands. The current sequence is that of the human collagen alpha(I) C-propeptide T2 construct protein of the invention. The construct includes a mutated BMP-1 recognition site but does not contain the glycine-repeat triple helical region.
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Matches 247; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 247 AA;
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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a first polypeptide to be trimerized, and introducing the construct into a clararyotic cell. Receptor decoys, e.g. soluble receptors consisting of culty the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much injer affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for maturally occurring trimeric ligands. The current sequence is that of the human soluble CD4-TRO of the invention. The collagen 12 fusion protein (GD4-T2) of the invention. The collagen T2 construct includes a mutated applying the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes a content of the broad and the construct includes and the construct of the construct of the construct
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signal peptide sequence followed by in-frame fusion to polypeptide to
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100.0%; Pred. No. 1e-126;
ive 0; Mismatches 0;
                                                                        SEQ ID NO 16; 47pp; English.
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nes 247; Conservative
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Synthetic.
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                           crimerized
                                                                          Claim 16;
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Matches
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AEA28579 standard; protein; 502 AA.

(first entry)

28-JUL-2005

AEA28579;

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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a first polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of culy the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of cury injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for naturally occurring trimeric ligands. The current sequence is that of the human placental alkaliae phosphatase (AP)-human collagen alpha (I) construct includes a mutated BNP-1 recognition site but does not contain
                                                                                                                                                                                                                                                                                                                                                                             Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
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                       /note= "Encoded by GA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; SEQ ID NO 8; 47pp; English.
                                                                                                                                              04-OCT-2004; 2004WO-US032753
                                                                                                                                                                                       02-OCT-2003; 2003US-00677877
                                                                                                                                                                                                                              (GENH-) GENHUNTER CORP.
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Misc-difference 509
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                                                              WO2005047850-A2
                                                                                                                                                                                                                                                                   Liang P;
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ö RSDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWID 568 YGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNRIB 688 YGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIE 180 IRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFD 240 PNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKAWYISKNPKDKRHVWFGESMTDGFQFB IRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFD RSDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWID PNOGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFE ; 0 Length 755; Indela 100.0%; Score 1329; DB 9; 100.0%; Pred. No. 1.4e-126; iive 0; Mismatches 0; Conservative VGPVCFL 247 Query Match Best Local Similarity 247; 181 509 61 699 121 629 241 Matches ద g 8 원 ∂ ሯ 셤 δ

Sequence 755 AA;

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Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
                                            Human soluble TNF-RII-collagen alpha(I) C-propeptide T2 fusion protein.
                                                            protein secretion; fusion protein; protein activation; collagen I; Tumor necrosis factor; TNF-RII; mutein.
                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 12; 47pp; English.
                                                                                                                                                   04-OCT-2004; 2004WO-US032753.
                                                                                                                                                                   02-OCT-2003; 2003US-00677877
                                                                                                                                                                                   (GENH-) GENHUNTER CORP.
                                                                                                                                                                                                                 WPI; 2005-386406/39.
N-PSDB; AEA28578.
                                                                                                                    WO2005047850-A2.
                                                                                     Homo sapiens
                                                                                                                                    26-MAY-2005.
                                                                                              Synthetic.
                                                                                                                                                                                                                                                                 trimerized
                                                                                                    Chimeric.
                                                                                                                                                                                                   Liang P;
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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion. to the polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of drug injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for maturally occurring trimeric ligands. The current sequence is that of the naturally occurring trimeric ligands alpha(1) C-propeptide T2 fusion protein (sTMF-T1) which is a protein (sTMF-T1-T2) and invention. The collagent to be the continuents. includes a mutated BMP-1 recognition site but does not contain the glycine-repeat triple helical region.

ö 257 SDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRRNFARTCRDLKMCHSDWKSGEYWIDP 316 61 2 SDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDP Gaps ö 0; Indels 100.0%; Pred. No. 2.4 ive 0; Mismatches Conservative Matches 246;

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VGPVCFL 755

749

99.6%; Score 1324; DB 9; Length 502; 100.0%; Pred. No. 2.4e-126;

Local Similarity

Query Match

Sequence 502 AA;

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307
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useful
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                                                             NQGCNLDAIKVPCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGBSMTDGFQFEY 376
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                                                                                                                                                                                                                                                                                       RAEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDV
                                NOGCINLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEY
                                                                                                                                           GGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEI
                                                                                                                                                                                                                                                       RAEGNSRFTYSVTVDGCTSHTGAWGKTVIBYKTTKSSRLPIIDVAPLDVGAPDQEFGFDV
                                                                                                                                                                         protein secretion; fusion protein; protein activation; collagen I.
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XX DE Huma
XX DE Homc
OS Synt
XX DE HOMC
OS Synt
XX DE HOMC
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              useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their maturally occurring trimeric ligands. The current sequence is that of the human collagen alpha(I) C-propebtide TO construct protein of the invention. The construct includes a partial glycine-repeat triple helical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 306
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a DNA construct comprising a promoter linked to a template encoding a
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/label= Human collagen alpha(I) glycine repeat region
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injections for each patient. The method of the invention may be
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                                                                                                                                                                         99.3%; Score 1320; DB 9;
100.0%; Pred. No. 3e-126;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 245; Conservative
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                                                                                                                                           Sequence 311 AA;
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The invention relates to a novel method for generating a secreted crimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide to be trimerized, which in turn is joined in-frame to a polypeptide to be trimerized, which in turn is joined in-frame to a polypeptide capable of self-trimerization which is heterologous to the first polypeptide to be trimerized, and introducing the construct into a cukaryotic cell. Receptor decoys, e.g. soluble receptors consisting of only the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much higher affinity to their ligand than their dimeric counterparts. Such rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of cutual injections for each patient. The method of the invention may be useful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their channer sequence is that of the name soluble TNP-RII-human collagen The current sequence is that of the human soluble TNP-RII-TO) of the invention. The collagen TO construct includes a partial glycine-repeat triple helical region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCCNLDAI KVFCNMETGETCVY PTQPSVAQKNWYI SKNPKDKRHVWFGESMTDGFQFEYG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGSDPADVAIOLTFLRLMSTEASONITYHCKNSVAYMDQQTGNLKKALLLKGSNEIFIR 501
peptide sequence followed by in-frame fusion to polypeptide to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 1320; DB 9; Length 566; 100.0%; Pred. No. 7.4e-126; ive 0; Mismatches 0; Indels 0
                                                                            Claim 15; SEQ ID NO 10; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322
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AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein secretion; fusion protein; protein activation; collagen 1; CD4.
                                                                     AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human soluble CD4-collagen alpha(I) C-propeptide T0 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEA28581 standard; protein; 699 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                           PVCFL 247
                                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                                                                                                                                   PVCFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2005
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     183
                                                                                                                   502
                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                   562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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110 AEA

120 AEA

XX AEA

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62

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634

183 AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 242 AEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 694

669 PVCFL 247

RESULT

391. .427 /label= Human collagen alpha(I) glycine repeat region

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243 695

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The invention relates to a novel method for generating a secreted trimeric fusion protein. The method comprises creating a DNA construct comprising a transcriptional promoter linked to a template encoding a signal peptide sequence followed, via an in-frame fusion, to the colypeptide to be trimerized, which in turn is joined in-frame to a colypeptide to be trimerized, which in turn is joined in-frame to a colypeptide to be trimerized, and introducing the construct into a creative to the tirst polypeptide to be trimerized, and introducing the construct into a contract cellular ligand-binding domain, may be used to intercept a conty the extracellular ligand-binding domain, may be used to intercept a ligand and thus overcome the overactivation of a receptor during disease treatment. Trimeric receptor decoys theoretically should have a much rationally designed soluble trimeric receptor analogs could significantly increase clinical benefits, as well as lower the amount or frequency of increase clinical benefits, as well as lower the amount or frequency of cuseful for generating a secreted trimeric fusion protein to be used for more efficient neutralization of the biological activities of their manners of the invention. The cultagen alpha(1) C-propeptide TO fusion protein (SCD4-TO) of the invention. The collagen TO construct includes a partial construct repeat triple helical region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 QGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR 182
                                                                                                                                                                                                                                                                                                                           Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be trimerized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 QCCNLDAIKVFCNMETGETCVYPTQPSVAQXNWYISKNPKDKRHVWFGESMTDGFQFEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
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                                                                                                   04-OCT-2004; 2004WO-US032753.
                                                                                                                                          32-OCT-2003; 2003US-00677877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 245; Conservative
                                                                                                                                                                                 (GENH-) GENHUNTER CORP
                                                                                                                                                                                                                                                                   2005-386406/39.
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                                                                                                                                                                                                                                                                                      N-PSDB; AEA28580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 699 AA;
                 WO2005047850-A2
                                                          26-MAY-2005
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63 QGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG

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                                                                                                                                                                                                                                    Human alkaline phosphatase-collagen alpha(I) C-propeptide fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generating a secreted trimeric fusion protein by introducing into a cell a DNA construct comprising a promoter linked to a template encoding a signal peptide sequence followed by in-frame fusion to polypeptide to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511. .548
/label= Human collagen alpha(I) glycine repeat region
                                                                                                                                                                                                                                                                                                     protein secretion; fusion protein; protein activation; collagen I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 819;
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100.0%; Pred. No. 1.3e-125;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; SEQ ID NO 6; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                      AEA28573 standard; protein; 819 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2004; 2004WO-US032753.
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                                                                                                                                                                                                                                                                                                                                        Alkaline phosphatase; enzyme
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENH-) GENHUNTER CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-386406/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2005047850-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                     28-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Chimeric.
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                                                                                                    AEA28573;
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Region
ABA28573

ABA28573

ABA28573

ABA2

ABA3

ABA3
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The invention relates to a novel isolated polynucleotide comprising any of the 235 nucleotide sequences described in the specification. The invention further comprises: an isolated polynucleotide encoding a playestic for the 235 nucleotide activity, where the polynucleotide hybridizes to polypeptide with biological activity, where the polynucleotide hybridizes to one of the 235 novel polynucleotides under stringent hybridization comprises than about 99% sequence identity with the novel polynucleotide; a vector comprising a novel polynucleotide; and captession vector comprise the novel polynucleotide, which can be operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell; an isolated cypreptide encoded by the novel polynucleotide, or a polynucleotide cypreptide encoded by the novel polynucleotide, or a polynucleotide; and carrier; an antibody composition comprising the polypeptide and a carrier; an antibody composition comprising the polypeptide and a carrier; an antibody directed against the polypeptide; a method for detecting the novel composition comprising the polypeptide; a method for identifying a compound that binds to the polypeptide is a method for identifying a compound that binds to the polypeptide; a method for producing the polypeptide; an isolated polypeptide in a sample; a method for identifying a compound that binds to the polypeptide is a method for producing the polypeptide; an isolated polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding a polypeptide with biological activity, useful for treating inflammation, leukemias, nervous system disorders, or infections.
                                                         182
                                                                                   antiinflammatory; cytostatic; antimicrobial; gene therapy; inflammation; leukaemia; nervous system disorder; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein factor discovery related isolated human polypeptide, SEQ ID 448.
123 GQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR
                                                                                                                                               183 AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG
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                                                                                                                                                                                                                                                                                                                                                                                     ADS98184 standard; protein; 1284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2004; 2004WO-US009202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-737686/72.
                                                                                                                                                                                                                                   247
                                                                                                                                                                                                                                                                           815 PVCFL 819
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                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                            ADS98184;
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Gaps

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0; Indels

Local Similarity 100. les 245; Conservative

Best Loca Matches

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575 DANVVRDRDLEVDTTLKSLSQOIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN 634

DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN

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                                                                                                                                                                                                                                                                                                                                                                               ABGNSRPTYSVTVDGCTSHTGAWGKTVIEVKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 242
comprising any of the 235 amino acid sequences described in the specification; and a collection above. The polymuclassing of at least one of the polymucleotides cited above. The polymptides and polymucleotides of the invention have antiinflammatory, cytostatic, and antimicrobial activities. The novel polymucleotide may be used to treat disorders by gene therapy. The polymptides and polymucleotides are useful for treating inflammation, leakemakes, nervous system disorders, or infections. This sequence represents one of the 235 novel isolated
                                                                                                                                                                                                                                                                        QCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                           GGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR 182
                                                                                                                                                                                                                                   1040 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                                                                   3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                                           Gaps
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                                                                                                                                                              99.3%; Score 1320; DB 8; Length 1284; 100.0%; Pred. No. 2.5e-125; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pro-alpha-1 chain of type I procollagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COL1Al gene; collagen; procollagen; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .22
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23. .1464
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB82454 standard; protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                         polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-398145/42.
N-PSDB; AAF90491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVCFL 1284
                                                                                                                                                                          al Similarity
245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     PVCFL 247
                                                                                                                                     Sequence 1284 AA;
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                                                                                                                                                               Query Match
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procollagen. The present invention relates to antisense oligonucleotides (ASOS) and their use in inhibiting expression of type I procollagen. The ASOS comprise 18-25 nucleotides and are complementary to a specific region within the type I collagen pro-alpha-1 chain gene (see AAF90491), especially those given in AAF90492-503. They are capable of inhibiting the expression of the pro-alpha-1 chain in a cell that expresses it. The ASOS are used in a claimed method of treating, or reducing a risk of, a collagen disorder. Such disorders may include those caused by overproduction of collagen fibres, such as liver cirrhosis, kidney, liver and heart fibrosis, scleroderma, hypertrophic scars and keloids
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     expression
and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG
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Novel antisense DNA oligonucleotide useful for inhibiting the of wild type COLIA1 gene, for treating, reducing the risk of, preventing collagen disorders.
                                                                                                                                                                                                                                                                                                                                         Length 1464;
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                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                         99.3%; Score 1320; DB 4; L 100.0%; Pred. No. 3.1e-125; Live 0; Mismatches 0;
                                                                       Disclosure; Page 21-26; 30pp; English
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11-APR-2001; 2001US-0282850P.
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Best Local Similarity 100.
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                            Sequence 1464 AA;
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30-JAN-2002; 2002WO-US002781
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                                                                                                                                                                                                                                                                                                 The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90749, ABB90749, ABB90760 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, neoanglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL93143-ABL92191; normal (PEM) ABL91903-ABL92104; and pan-endothelial markers
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                                                                                                                                                                An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%; Score 1320; DB 5; Length 1464; 100.0%; Pred. No. 3.1e-125; cive 0; Mismatches 0; Indels 0
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                                                 Vogelstein B;
                                                                                                                                                                                                                                                              Claim 54; Page 265-268; 331pp; English.
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                                               St Croix B, Kinzler KW,
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                                                                                              WPI; 2002-291856/33
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                                                                                                                    N-PSDB; ABL92119
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ABP68610
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AC ABP68
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AC ABP68
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately tringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-CAPR6837) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polymocleotides, antibodies, tusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polymucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
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                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ, Persing DH, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 159; 300pp + Sequence Listing; English
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30-JAN-2001; 2001US-0265305P.
31-JAN-2001; 2001US-0265682P.
09-FEB-2001; 2001US-0267568P.
21-MAR-2001; 2001US-0278651P.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0391631P.
12-JUL-2001; 2001US-0333626P.
27-NOV-2001; 2001US-0333626P.
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Matches 245; Conservative
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NO:65.

(first entry)

1460 PVČFL 1464

PVCFL 247

243

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Breast cancer associated protein sequence SEQ ID
                                                                                                                                                                                                         Human; breast cancer; cytostatic; gene therapy
                                                                                                    ABR47417 standard; protein; 1464 AA.
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14-MAY-2002; 2002US-0380391P
                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENIUM PHARM INC
                                                                                                                                                                                                                                                            WO2003004989-A2.
                                                                                                                                                      12-JUN-2003
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                          21-JUN-2001;
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                                                                                                                                                                                                                                                                                      16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lillie J, Mertens M,
                                                                                                                              ABR47417;
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                                                                                                                                                                                                                                                                                                                                                                                                                   New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoanglogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present
                                                                                     Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; pan-entopathy; rheumatoid arthritis; tumour anglogenesis; neoanglogenesis; immune response; cytostatic; antidiabetic, ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a human TEM or NEM protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%; Score 1320; DB 6; Length 1464; 100.0%; Pred. No. 3.1e-125; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                      Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying candidate drugs for treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 295-297; 374pp; English.
                                                              endothelial marker TEM 38
                                                                                                                                                                                                                                                                                                                                                      St Croix B,
                                                                                                                                                                                                                                                            10-APR-2002; 2002WO-US008253.
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36-FEB-2002; 2002US-0354262P.
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                                    (first entry)
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Best Local Similarity 100.
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Carson-Walter E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1464 AA;
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                                                                                                                                                                                                         WO200283874-A2.
                                                              Human tumour
                                                                                                                                                                                                                                                                                                  06-FEB-2002;
                                                                                                                                                                                  sapiens
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Meyers RE;

Kamatkar S; Zhao X, Meyers R Sahin A, Mills GB;

t, Hoersh S, Kamatkar Wang Y, Xu Y, Zhao X, L, Meric F, Sahin A,

Myer V, Wan Pusztai L,

Glatt K,

Gannavarapu M, Monahan JE, N Hortobagyi GN,

2001US-0301572P. 2001US-0306501P. 2001US-0325002P.

2001US-0299887P.

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                                                                                                   expression
                                                                                                                                                                                                                                                                                 The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC5034 and ABR47386 to ABR4738) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a pignificant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRXNPARTCRDLKMCHSDWKSGEYWIDPN
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                                                                               Breast cancer diagnosis or treatment by comparing the level of expri
of a marker in a patient sample with that in the control non-breast
cancer sample.
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100.0%; Pred. No. 3.1e-125;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                               Claim 1; SEQ ID NO 65; 128pp; English.
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   2003-210381/20.
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les 245; Conserv
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WPI; 2003-210381/
N-PSDB; ACC50108.
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1280 QGCNLDAIKVFCNWETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 1339

QGCNLDAIKVPCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122

DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN 1279

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DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN

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GOGSDPADVAIOLTFLRLMSTEASONITYHCKNSVAYMDOOTGNLKKALLLKGSNEIEIR

1400 AEGNSRPTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 1459

AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 242

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1400 AEGNSRPTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
                                                                                                                                                                                                         AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cervical cancer; cervical cancer marker; cancer therapy; detection; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen Y, Zhao X, Monahan JE, Kamatkar S;
M, Glatt K, Hoersch S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cervical cancer cell marker protein SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 164-167; 386pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR92064 standard; protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-2001; 2001US-0298155P.
13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
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N-PSDB; ACF12845.
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| PVCFL 1464
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Sequence 1464 AA

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                                                                                                                                                                                                                                                                                                                                                                                                               123 GQGSDPADVAIQLIFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLLKGSNEIEIR
                                                                          .<u>`</u>
Query Match 99.3%; Score 1320; DB 6; Length 1464; Best Local Similarity 100.0%; Pred. No. 3.1e-125; Matches 245; Conservative 0; Mismatches 0; Indels 0
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Job time : 64.6272 secs
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given in ABR92047 to ABR92164. A higher level of expression of (I) than

corrmal indicates the presence of cervical cancer. Also described: (I) a

vector (II) containing (I); (2) a host cell (III) containing (I); and (3)

cassessing (MI) whether a patient is afflicted with cervical cancer,

comprising comparing the level of expression of a marker in a patient's

sample, and the normal level of expression of the marker in a control non

cervical cancer sample, where a significant increase in the level of

corrical cancer in the patient's sample relative to that in the

control sample is an indication that the patient is afflicted with

cervical cancer. (I) has cytostatic activity, and can be used in gene

therapy and in vaccines. (I) is useful in detecting, characterising,

therapy and treating human cervical cancers. (I) may also be used in

various prognostic and diagnostic assays, pharmacogenomics and in

monitoring clinical trials
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                     Copyright
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OM protein - protein search, using sw model

Run on:

April 26, 2006, 16:14:30 ; Search time 22.5753 Seconds (without alignments) 1052.725 Million cell updates/sec

1 RSDANVVRDRDLEVDTTLKS......LDVGAPDQEFGFDVGPVCFL 247 US-10-677-877A-4 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: * PIR_80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	alpha 1							alpha	alpha	II A1	alpha	alpha 1(		alpha 2(	alpha 1(	alpha 1(		alpha 2(	alpha 1(	lpha 2	aJ	procollagen type V	lpha 1	collagen alpha 1(I	alpha 1	alpha 1			
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مد	Match	98.6	92.2	91.6	75.7	73.9	73.7	72.8	72.8	71.2	70.5	6.69	66.4	66.4	66.4	64.7	64.3	64.2	64.2	64.1	59.9	56.8	56.0	53.8	49.9	œ	æ	ø	37.7	37.6
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632	1414	482	3198	1051	91	547	1546	193	69	39	31	37	21	293	884
37.3	37.2	36.8	35.4	29.9	26.6	26.5	23.4	21.9	19.7	15.3	10.2	7.6	7.8	6.8	6.7
496	495	488.5	471	397.5	353	352.5	311	291	262	203	136	129	104	90	89
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## **ALIGNMENTS**

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Collagen alpha 1(I) chain precursor - human

NiAlternate names: procollagen alpha 1(I) chain

C;Species Homo sapiens (man)

C;Species Homo sapiens (man)

C;Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 31-Dec-2004

C;Accession: IG0114; S0114; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11

S;G9; A29439; I53466; A02852; I37247

R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.

Gene 67, 105-115, 1988

A;Title: Complete nucleotide sequence of the region encompassing the first twenty-five e:

A;Reference number: IG0114; WUID:88329734; PMID:2843432
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A; Status: translated from GB/EMBL/DDBJ

A, Molecule type: DNA A, Residues: 1-369, 'L', 371-589 < DAL> A, Cross-references: UNIPROT: P02452; UNIPROT: Q14992; UNIPROT: Q16053; UNIPROT: Q13896; UNIP. R, Tromp, G, Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock. Biochem. J. 253, 919-922, 1988 A, Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human A, Reference number: S01143; MUID: 89025644; PMID: 3178743

, Accession: S01143

A; Molecule type: mRNA A; Residues: 1-472 < TRO> A; Residues: 1-472 < TRO> A; Cores = Tefernces: UNIPPRC: UPI000016A6F9; EMBL: X07884; NID: 930015; PIDN: CAA30731.1; PID A; Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988 R; Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.; Nature 310, 337-340, 1984

A;Title: Human proalphal(I) collagen gene structure reveals evolutionary conservation of A;Reference number: A93335; WUID:84270697; PMID:6462220 A;Accession: A93335

A; Molecule type: DNA
A; Molecule type: DNA
A; Residuces: 1-86, Q', 60-181 < CHU>
A; Residuces: 1-86, Q', 60-181 < CHU>
A; Cross-references: UNIPARC: UDIO000173B3C; EMBL: X00820; NID: 935657; PIDN: CAA25394.1; PID
B; Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W., Biol. Chem. 262, 15151-15157, 1987
A; Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh
A; Reference number: 155254; MUID: 88033098; PMID: 2822714

A; Status: translation not shown; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-45 < ROS> A; Accession: I55254

A;Cross-references: UNIPARC:UPI000016A6B2; GB:J02829; NID:g180387; PIDN:AAA51993.1; PID: R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E. Proc. Natl. Acad. Sci. US.A. 84, 8869-8873, 1987.
A;Title: Regulatory elements in the first intron contribute to transcriptional control o A;Reference number: A39943; MUID:88097389; PMID:3480516

A;Molecule type: DNA A;Residues: 1-34 *BORx-A;Cross-references: UNIPARC:UPI000016A6B1; GB:J03559; NID:g180876; PIDN:AAA52052.1; PID: R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A;Molecule type: mRNA
A;Residues: 1179-1336,1339-1464 <CH6>
A;Cross-references: UNIPARC:UP10000173B4E
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A; Residues: 1179-1464
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A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter s A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter s A;Reference number: I5537; MUD:85130970; PMID:2857713
A;Refatus: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-34 CCH2.
A;Residues: 1-34 CCH2.
A;Residues: 1-34 CCH2.
A;Residues: 1-34 CCH2.
A;Cross-references: UNIPARC:UPI000016A6B1; GB:M10627; NID:9180383; PIDN:AAA51992.1; PID: R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist J. Biol. Chem. 265, 6312-6317, 1990
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Appendues: 281-302/402-27022-242-2515-5441202-54410254 CALBA Appendues: 281-302/402-27022-5415-55-5441202-44855, UNIPARC.UPDO000173844; MARC.UPDO00173844; UNIPARC.UPDO00173844; UNIPARC.UPDO00173844;
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Collagen alpha 1(1) chain precursor - mouse Cipagen was musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 557243; S16374; \(\bar{A}\)Z23982; I49559; I49557; S39789; I48300; S21626
R; Li, S; W.; Khillan, J.; Prockop, D.J.
Matrix Biol. 14, 593-595, 1994
A; Title: The complete CDNA coding sequence for the mouse pro-alpha-1(I) chain of type I and the complete of the mouse pro-alpha-1(I) chain of type I and the constant of the mouse pro-alpha-1(I) chain of type I are complete of the mouse pro-alpha-1(I) chain of type I are complete of the mouse pro-alpha-1(I) chain of type I are complete of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of the mouse pro-alpha-1(I) chain of the mouse pro-alpha-1(I) chain of type I are constant of the mouse pro-alpha-1(I) chain of the mouse pro-alpha
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-25 < RE2>
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A;Rolecule type: DNA
A;Residues: 1-80, E', 82-105, 'D', 107-185;1031-1201, 'G', 1203-1218, 'E', 1220-1221, 'T', 1223-12, A;Residues: 1-80, E', Rippe, R.A.; Türpeye, R.A.; Türzeye, R.A.; Nehls, M.; Brenner, D.A.; Breindl, M.
A;Title: DNA methylation represses the murine alpha 1(1) collagen promoter by an indirect A;Reference number: 148300; MUID:94344105; PMID:8065328
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A;Residues: 1-80,'E',82-105,'D',107-147 <REF>
A;Cross-references: UNIPARC:UP1000017738B; EMBL:X54876; NID:950486; PIDN:CAA38657.1; PID
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A; Residues: 1-1453 <LIS.
A; Cross-references: UNIPROT: P11087; UNIPARC: UPI0000027558; EMBL: U08020; NID: g470673;
R; Meteascanta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
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A; Reference number: S16176; MUID: 91274355; PMID: 2054384
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A;Molecule type: DNA
A;Residues: 1442-1453 <MET>
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A; Residues: 518-1128 < FRE>
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: 150629
B;Fuller, F.; Boedtker, H.
Bacchemiastry 20, 996-1006, 1981
A;Fuller, Sequence determination and analysis of the 3' region of chicken pro-alpha 1(1)
A;Fuller: Sequence determination and analysis of the 3' region of chicken pro-alpha 1(1)
A;Facters number: 150629
A;Accession: 150629
A;Accession: 150629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-473 <FUL>
A;Residues: 1-473 <FUL>
A;Residues: 1-473 <FUL>
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; F;244-473/Domain: fibrillar collagen carboxyl-terminal homology;
A;Experimental source: fetal cell 86-146
A;Accession: E44426
A;Accession: E47426
A;Moslocule type: mRNA
A;Residues: 1179-1387,'R',1389-1464 <CH7>
A;Cross-references: UNIPARC:UPI000017384F
A;Experimental source: fetal cell 88-251
B;Cohn, D.H.; Apone, S; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nic J. Biol. Chem. 263, 14605-14607, 1988
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3; Mismatches 0;
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Matches 218; Conservative
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Best Local Similarity 98.8
Matches 242; Conservative
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A, Accession: A38513
A, Molecule type: DNA
A, Residues: 1-103 < RYA>
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Collagen alpha 1(II) chain precursor - chicken (fragment)
Collagen albuba gallus chicken)
Collagen albuba gallus chicken
Alfles structure and sequence of the chicken type II procollagen gene. Characterizatic
Alfles structure and sequence of the chicken type II procollagen gene. Characterizatic
Alfles structure and sequence of the chicken type II procollagen gene. Characterizatic
Alfles sequence corresponds to the last four eaxons
Riyoung M.F. vogel, in G. Numae, A.M.; Fernandez, M.P.; Sullivan, M.; Sobel, M.E.
Alfles sequence corresponds to the last four eaxons
Riyoung M.F. vogel, in G. Numae, A.M.; Fernandez, M.P.; Sullivan, M.; Sobel, M.E.
Alfles contacts on the sequence corresponds to the last four encoding type II collagen.
Alfles sequence corresponds to the last four eaxons
Riyoung M.F. vogel, in State and State an
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; triple helix F;1-22/Domain: signal sequence #status predicted <SIG> F;23-15/Domain: amino-terminal propeptide #status predicted <PRO> F;30-89/Domain: won Willebrand factor type C repeat homology <WC> F;10-89/Domain: von Willebrand factor type C repeat homology <WC> F;122-1453/Product: collagen alpha 1(I) chain #status predicted <WAT> F;1224-1453/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1269 QGCNLDAIKVYCNMETGQTCVFPTQPSVPQKNWYISPNPKGKKGHVWFGESMTDGFPFFYG 1328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 GQGSDPADVAIQLTFIRIMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIBIR 182
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                                                                                                                                                                                                                                                                                                                                                                                                                       3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
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Matches 220; Conservative
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NiAlternate names: procollagen alpha i(II) chain
NiContains: chondrocalcin; collagen alpha i(II) chain precursor splice form 1; collagen &
Cispecies: Homo sapiens (man)
Cipate: 28-May-1986 #sequence revision 01-Sep-1995 #text change 31-Dec-2004
Cipate: 28-May-1986 #sequence revision 01-Sep-1995 #text change 31-Dec-2004
Cipate: 28-May-1986 #sequence revision 01-Sep-1995 #text change 31-Dec-2004
Cipate: 137251; 137252; 137253; 137254; 155338; 159535; 161910
R.Ryan, M.C.; Siersaki, M.; Sandell, L.J.
Agritle: The human type II procollagen gene: identification of an additional protein-codi
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: UNIPARC: UP10000126D15; EMBL: X16468; NID: g29515; PIDN: CAA34488.1; PID
A; Note: alternative splice form 1
A; Note: alternative splice form 1
A; Note: alternative splice form 1
B; Vikkula, M.; Metsaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L.
Biochem. J. 285, 287-294, 1992
A; Title: Structural analysis of the regulatory elements of the type-II procollagen gene. A; Reference number: S24270; MUID: 92344585; PMID: 1637314
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A;Molecule type: DNA
A;Residues: 1-28 <VIX>
A;Residues: 1-28 <VIX>
A;Cross-references: UNIPARC:UP10000173B64; EMBL:X58709; GB:S40537; NID:g35659
A;Note: this translation is not annotated in GenBank entry HSPROCOB1, release 111.0
Gene 44, 11-16, 1986
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                                 F;42-43/Cleavage site: Ala-Asp (procollagen C-endopeptidase) #status experimental F;189/Binding site: carbohydrate (Asn) (covalent) #status predicted F;194-239/Disulfide bonds: #status predicted
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Nucleic Acids Res. 17, 9473, 1989
A; Title: Nucleotide sequence of the full length cDNA encoding for human type II
A; Reference number: S06715; MUID: 90067946; PMID: 2587267
                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                   101 IDPNQGCTLDAIKVFCNMETGETCVYPTPSSIPRKNWWTSKT-KDKKHVWFAETINGGFH 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 FEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 238
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                                                                                                                                                                                                                                                                                   3.
60-288/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                    DB 1; Length 288;
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                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                               Query Match 75.7%; Score 1006.5; DB Best Local Similarity 70.3%; Pred. No. 5.6e-80; Matches 175; Conservative 37; Mismatches 34
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280 VDIGPVCFL 288
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A,Molecule type: DNA
A;Residues: 630-640, A',642-785 <VIX2>
A;Residues: 630-640, A',642-785 <VIX2>
A;COSS-references: UNIPARC: UPIO000173B6E; EMBL:X16158; NID:G29951; PIDN:CAA34278.1; PID
A34282.1; PID:G1335022; PIDN:CAA34283.1; PID:G1335023; PIDN:CAA34284.1; PID:G1335024
R;Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D
A; Biol. Chem. 252.222526, 1992
A;Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain pro-
A;Reference number: A44309; MUID:93054548; PMID:1429602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 752-831, PA', 834, F', 836-1005, K', 1007-1036, 'Q', 1038-1052, 'E', 1054-1068, 'T', A; Residues: 752-831, 'PA', 834, 'F', 836-1005, 'K', 1007-1036, 'Q', 1038-1052, 'E', 1054-1068, 'T', A; Cross-references: UNIPARC:UPI000017386F; GB:L00977; NID:3180812; PIDN:AAB23914.1; PID: A; Note: sequence extracted from NCBI backbone (NCBIP:117273); parts of this sequence wer A; Note: this translation is not annotated and this publication is not cited in GenBank e. A; Note: mutant sequence associated with perinatal lethal hypochondrogenesis R; Tiller, G.B.; Rimoin, U.L.; Murray, L.W.; Cohn, D.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3889-3893, 1990
A; Title: Tandem duplication within a type II collagen gene (COL2A1) exon in an individua A; Reference number: $16502; MUID:90251662; PMID:2339128
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A; Mesidues: 1023-1056, 'N', 1058-1068, 'T', 1070-1487 < CHE>
A; Cross-references: UNIPARC: UP1000016A6BB; GB: J00116; NID: g180395; PIDN: AAA51997.1; PID::
R; Elima, K.; Vuorio, T.; Vuorio, E.
R; Elima, K.; Vuorio, T.; Vuorio, E.
A; Elima, K.; Vuorio, T.; Vuorio, E.
A; Title: Determination of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the human pro-alpha-1(II) control of the single polyadenylation site of the single poly
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A; Residues: 1175-1487 < ELI.>
A; Residues: 1175-1487 < ELI.>
A; Cross-references: UNIPARC: UPI000016A71B; EMBL: X06268; NID: 930096; PIDN: CAA29604.1; PID
A; Experimental source: fetal epiphyseal cartilage
R; van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
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A; Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
A; Reference number: A57033; WUID: 87099927; PMID: 3800925
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A; Molecule type: protein

A; Residues: 'XE',1244-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 «VAN»

A; Cross-references: UNIPARC:UPI0000173B70; UNIPARC:UPI0000173B71; UNIPARC:UPI0000173B72

A; Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prop

R; Strom, C.M.; Upholt, W.B.

R; Strom, C.M.; Upholt, W.B.

A; Reference number: A21733; MUID:84118798; PMID:6320112
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A;Cross-references: UNIPARC:UPI000016A61A; EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CA
A;Accession: B21733
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A;Residues: 884-909, PE' <STR2>
A;Cross-references: UNIPARC:UPI000006EA4D; GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g3
R;Nunez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6548, 1985
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A,Cross-references: UNIPARC:UPI000011F7F2; EMBL:M37126; NID:g180808; PIDN:AAA52037.1;
A,Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R;Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 2555-2559, 1985
A;Title: Identification and characterization of the human type II collagen gene (COL2A), Reference number: A02858; MUID:85190534; PMID:3857598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A44309
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                         number: $05000; MUID:89325561; PMID:2753125
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A,Residues: 1296-1358 <NUN2>
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                                                                                                       Accession: S05000
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A; Residues: 1-8,'T', 10-28 «NUN»

A; Cross-references: UNIPARC:UPI000016A71A; GB:M25698; NID:g180872; PIDN:AAA52051.1; PID: R; Baldwin, C. T.; Reginato, A.M.; Smith, C.; Jimenez, S.A.; Prockop, D.J.
Biochem. J. 262, 521-528, 1989

A; Title: Structure of cDNA clones coding for human type II procollagen. The alpha-1(II)
A; Accession: 806496

A; Molecule type: mRNA
A; Residues: 728,'R', 99-157,'P', 159-440,'G',442-456,'E',458-640,'A',642-831,'PA',834,'F',A; Cross-references: UNIPARC:UPI000013B65; EMBL:X16711; NID:g30040; PIDN:CAA34683.1; PID
A; Mote: alternative splice form 1
A; Mote: alternative splice form 2
A; Accession: A35428
A; Accession: A35428
A; Accession: A35428
A; Residues: 27-81,'L', A3-103 arxA2>
A; Cross-references: UNIPARC:UPI0000173B66
A; Mote: alternative splice form 2; splicing appears to be under developmental regulation A; Mote: alternative splice form 2; splicing appears to be under developmental regulation B; M; M; Benson-Chanda, V; Vissing, H.; Ramirez, F.
Genomics 4, 438-41, 1989
A; Reference number: A30147; MUID:89233138; PMID:2714801
A; Reference number: A30147; MUID:89233138; PMID:2714801
A; Reference number: A30147; MUID:89233138; PMID:2714801
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A,Molecule type: DNA
A,Residues: 440, 'G', 442-456,'E', 458-480,'P', 482-509 <TILI>
A,Residues: 440, 'G', 10000006734, EMBL: U15195; NID: G557053; PIDN: AAB60370.1; PI
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A; Residues: 171-172, CC, 174-175 < ALA>
A; Cross-references: UNIPARC: UP10000173B68
A; Note: mutant sequence from a family with family with primary generalized osteoarthriti
R; Diab, M; Wu, J.J; Byre, D.R.
B; Diab, M; Wu, J.J; Byre, D.R.
B; Diab, M; Wu, J.J; Syre, D.R.
A; Title: Collagen type: Trom human cartilage: a structural profile of intermolecular of A; Reference number: S64673; MUID: 96195147; PMID: 8660302
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A; Molecule type: protein
A; Molecule type: protein
A; Cross-references: UNIPARC: UP1000017386B; UNIPARC: UP10000173B6D
A; Cross-references: UNIPARC: UP1000017386B; UNIPARC: UP10000173B6D
B; Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, Am. J. Hum. Genet. 56, 388-395, 1995
A; Tiller, An RNA-splicing mutation (G+51VS20) in the type II collagen gene (COL2A1) in a A; Reference number: I38867; MUID: 95150028; PMID: 7847372
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A;Residues: 501-676,'A',678-783,'A',785-831,'PA',834,'F',836-1214 <RAM>
A;Cross-references: UNIPARC:UF1000016A700; EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PIQ
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A; Molecule type: protein
A; Residues: 188-189, 'X', 191-195;1224-1230,'X', 1232-1236 < DIA>
A; Residues: 188-189, 'X', 191-195;1224-1230,'X', 1232-1236 < DIA>
A; Cross-references: UNIPARC: UP10000173869; UNIPARC: UP1000017386A
B; Franc, S.; Marzin, B.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, Bur J. Biochem. 234, 125-131, 1995
A; Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil car A; Reference number: S63514; MUD: 96096730; PMID: 8529631
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A;Residues: 104-157, P',159-236 <SUM>
A;Residues: 104-157, P',159-236 <SUM>
A;Cross-references: UNIPARC:UPI0000173B67; GB:J03065; GB:M23660; GB:M25655; GB:M25656;
A;Cross-references: UNIPARC:UPI0000173B67; GB:J03065; GB:M2560; D.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6565-6568, 1990
A;Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of px A;Reference number: A94227; MUID:90370826; PMID:1975693
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FRBS Lett. 250, 171-174, 1989
A,Title: Structural analyses of the polymorphic area in type II collagen gene.
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A;Reference number: S04892
A;Accession: S04892
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PI

(COL2A1)

238

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CyAccession: A41182; Assquare_reversion. B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A;Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and & A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Recession: A41182
A;Recession: A41182
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1419 < MRTP.
A;Cross-references: UNIPARC:UPI0000177381; GB:M65161
A;Cross-references: UNIPARC:UPI0000177381; GB:M65161
A;Reference number: A44885; MUID:91347939; PMID:1879363
A;Reference number: A44885; MUID:91347939; PMID:1879363
A;Reference number: A44885
A;Reference number: A44885
A;Rolecule type: DNA
A;Residues: 1-28 < CCHE>
A;Residues:
                                                             1297 NLAPNTANVQMTFLRLLSTEGSQNITYHCKNSIAYLDBAAGNLKKALLIQGSNDVEMRAE 1356
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                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(II) chain precursor - mouse
C,Species: Mus musculus (house mouse)
C,Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
                                                                                                                                     179 IBIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTKSSRLPIIDVAPLDVGAPDQEFG
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                                     PEYGGOGSDPADVAIOLTFLRLMSTEASONITYHCKNSVAYMDQQTGNLKKALLLKGSNE
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72.8%; Score 967.5; DB 2; Length
Best Local Similarity 68.3%; Pred. No. 1e-75;
Matches 166; Conservative 39; Mismatches 37; Indels
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|1410 VDIGPVCFL 1418
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A;Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A;Note: the codons given for 133-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the A;Note: the codons given for 133-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the Nucleic Acids Res. 13, 2207-2225, 1985
A;Title: Isolation and partial characterization of the entire human pro alpha 1(II) coll A;Refedence number: I37249; MUID:85215609; PMID:2987845
A;Residues: 7-28;R',99-114;511-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-1 A;Recsaion: 184453
A;Accession: 184453
A;Accession: I84453
A;Action Light Lyne (GB/EMBL/DDBJ)
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A;Residues: 7-28 <SANZ>
A;Crose.references: UNIPARC:UPI0000071780; UNIPARC:UPI0000173B74; UNIPARC:UPI0000173B75;
24938; NID:930104
A;Note: the GenBank PID is based on an incorrect reading frame
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69.1%; Pred. No. 5.3e-77;
cive 36; Mismatches 38
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Matches 172; Conservative
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Matches 172; Conservative
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VDIGPVCFL 1487
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A, Residues: 1-464 <YAN>
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A, Cross-references: UNIPROT. Q90412; UNIPARC: UPI00000FC847; EMBL: U23822; NID: 9773660; PID: C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; F; 236-464/Pomain: fibrillar collagen carboxyl-terminal homology; P; 236-464/Pomain: fibrillar collagen carboxyl-terminal homology <PCC.
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Ribu, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115; 555-575, 1991
A.Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis emi A.Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis emi A.Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis emi A.F. Accession: A40333
A.F.
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Ryan, Y.; Hotta, K.; Riggleman, B.; Postlethwait, J.H.
Ryan, Y.; Hotta, K.; Riggleman, B.; Postlethwait, J.H.
Rubmitted to the EMBL Data Library, March 1995
A; Reference number: S59513
A; Reference number: S59513
A; Reference number: S59513
A; Retence number: Rybe II collagen gene in the zebrafish embryonic axis.
A; Retence number: S59513
A; Roterus: preliminary
A; Molecule type: mRNA
             1371 NIQMTFLRLLSTDASQNITYHCKNSIAFMDEASGNLKKAVLLQGSNDVEIRAEGNSRFTY 1430
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                                                                                                                                  collagen II A1 protein - zebra fish (fragment)
C;Species: Brachydanio rerio (zebra fish)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen alpha 1'(II) chain precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG
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70.5%; Score 937.5; DB 2; Length
Best Local Similarity 67.5%; Pred. No. 1e-73;
Matches 168; Conservative 34; Mismatches 44; Indels
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R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A.Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Accession: B41182
A;Accession: A;Accessi
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A; Residues: 1-1486 <SUA>
A; Cross-references: UNIPROT:091718; UNIPROT:091717; UNIPARC:UPI0000173B50; GB:M63595
A; Cross-references: UNIPROT:091718; UNIPROT:091717; UNIPARC:UPI0000173B50; GB:M63595
C; Superfamily: collagen alpha 1(1) chain; fibrillar matrix; glycoprotein; trimer; triple helix
P;37-96/Domain: von Willebrand factor type C repeat homology <VWC>
F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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A;Cross-references: UNIPROT:P02467; UNIPARC:UPI00001712EA; GB:M25963; NID:g211581; PIDN:JA;Cross-references: UNIPROT:P02467; UNIPARC:UPI00001712EA; GB:M25963; NID:g211581; PIDN:JA;Accession: 150207
A;Accession: 150207
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: UNIARC:UPI00001712AA; GB:M25965; NID:g211583; PIDN:AAA69961.1; PID:gR;Aho, S: Tate, V; Boedtker, H.
Nucleic Acids Res. 12, 6117-6125, 1984
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A;Residues: 128-161 <YA2>
A;Cross-references: UNIPARC:UP100001712A9; GB:J00828; NID:g211295; PIDN:AAA51612.1; PID:g
A;Accession: 150625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1.33 cAHO>
A,Residues: 1.33 cAHO>
A,Cross-references: UNIPPARC:UPI0000173BAC; EMBL:X00760; NID:g63266; PIDN:CAA25330.1; PID:
R,Tate, V.E.; Finer, M.H.; Boedtker, H.; Doty, P.
Nucleic Acids Res. 11, 91-104, 1983
A,Title: Chick pro-alpha-2 (1) collagen gene: exon location and coding potential for the A,Reference number: S10480; MUID:83246518; PMID:6135195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;MOlecule type: mENA
A;Residues: 1-89 <TAT>
A;Cross-references: UNIPARC:UP100001712EC; EMBL:X02657; NID:g63314; PIDN:CAA26493.1; PID:
A;Accesion: S10480
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R;Yamada, Y.; Avvedimento, V.E.; Mudryj, M.; Ohkubo, H.; Vogeli, G.; Irani, M.; Pastan, Edl 12, 887-892, 1980
A;Title: The collagen gene: evidence for its evolutinary assembly by amplification of a A;Reference number: ISO170; MUID:81112157; PMID:7460017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Location of the 11 bp exon in the chicken pro alpha-2(I) collagen gene.
Reference number: S07354; MUID:84297217; PMID:6473103
Recession: S07354
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule : 572-601 < YA4>
A;Cross-references: UNIPARC:UPIO000173BBO; EMBL:V00398; NID:g63299; PID:g833610
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A; Residues: 433-483 <YA5>
A; Cross-references: UNIPARC: UP1000001087; EMBL: V00394; NID: 963287; PID: 9833608
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A;Molecule type: DNA
A;Residues: 530-558 </A3>
A;Residues: 530-558 </A3>
A;Cross-references: UNIPARC:UP100000173BAF; EMBL:V00396; NID:g63295; PID:g833609
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A;Molecule type: DNA
A;Residues: 126-161 <XAM>
A;Residues: 126-161 <XAM>
A;Cross-references: UNIPARC:UPI00001712A9; EMBL:V00400; NID:g63305; PID:g833611
A;Accession: 150170
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A; Residues: 17-73 < TAWN
A; Cross-references: UNIPARC:UP10000173BAD
A; Cross-references: UNIPARC:UP10000173BAD
A; Cross-references: UNIPARC:UP10000173BAD
A; Orose: the authors translated the codon CAG for residue 42 as Glu
B; Vogeli, G.; Ohkubo, H.; Sobel, M.E.; Yamada, Y.; Pastan, I.; de Crombrugghe,
Proc. Natl. Acad. Sci. U.S.A. 78, 5334-5338, 1981
A; Title: Structure of the promoter for chicken alpha-2 type I collagen gene.
A; Reference number: S11146; MUID:82060240; PMID:6946474
R;Boedtker, H.; Finer, M.; Aho, S.
Ann. N. Y. Acad. Sci. 460, 85-116, 1985
A;Title: The structure of the chicken alpha 2 collagen ;
A;Reference number: ISO206; MUID:86185168; PMID:3868961
A;Accession: ISO206
A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-245 <BOE>
A;Cross-reference: Three
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A; Molecule type: DNA
A; Residues: 1-15 < VOG>
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CGCH28
collagen alpha 2(I) chain precursor - chicken (fragments)
c;Species Gallus gallus (chicken)
C;Date: 24-Apr-1984 #sequence revision 15-Aug-1997 #text change 09-Jul-2004
C;Accession: 150206; I50207; $07354; S10848; S10480; S11146; I50628; I50170; I50625; I50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A51305
A51305
A51305
Collagen alpha 1(II) chain - golden hamster (fragments)
Collagen alpha 1(II) chain - golden hamster)
Collagen areatus (golden hamster)
Collagen areatus (golden hamster)
Collagen areatus Mesocrictus auratus (golden hamster)
Collagen Mesocrictus auratus (golden hamster)
Collagen: Mesocrictus auratus
Collagen: A51396
Mol. Carcinog. 4, 14-24, 1391
Apritle: Loss of a tumor suppressor gene function is correlated with downregulation of Confederate number: A61396
Aprecession: A61396
Aprecession: A61396
Aprecession: A61396
Aprecession: A61396
Aprecession: Apr
                                                                                                                                                                                           1425 BIRAEGNSRFTYNALEDGCKKHTGKWSKTVIEYRTQKTSRLPIVDIAPMDIGGADQEFGV 1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 SRPTYTALKDGCTKHTGKWGKTVIEYRSQKTSRLPIIDIAPMDIGGFEQEFGVDIGPVCF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYGGQGS 126
                                                                                                                                                 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGF
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                                                                                                                                                                                                                                                                                                           DPNOGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQF
                                                                                                                                                 RSDANVVRDRDLEVDTTLKSLSQQIEN-IRSPEGSRKNPARTCRDLKMCHSDWKSGEYWI
                                                                  Gaps
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                                                                  IndelB
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thes 36;
                             64.9%; Pred. No. 2.4e
ive 47; Mismatches
                                                                  161; Conservative
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                             Similarity
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                        Best Local
Matches 16
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Aintrons: 24(1; 27/3; 33/3; 45/3; 73/3; 92/3; 107/3; 125/3; 143/3; 161/3; 179/3; 197/3; Aintrons: 24(1; 27/3; 33/3; 45/3; 73/3; 92/3; 107/3; 125/3; 143/3; 161/3; 179/3; 197/3; Aintrons: 24(1; 27) chain; fibrillar collagen carboxyl-terminal homology cylebratually: collagen alpha 2(1) chain; fibrillar matrix; glycoprotein; hydroxypy F;1-22/Domain: signal sequence #status predicted <SIG>F;23-77/Domain: anino-terminal propeptide #status predicted <PRO>F;78-954/Product: collagen alpha 2(1) chain (fragments) #status predicted <MATN>F;78-954/Product: collagen alpha 2(1) chain (fragments) #status predicted <MATN>F;78-954/Domain: fibrillar collagen carboxyl-terminal homology <PCC>F;78/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carbox)F;78/Modified site: allysine (Lys) #status experimental F;83/Modified site: 4-hydroxyproline (PrO) #status experimental F;866/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 2(1) chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 23-May-1997
C;Accession: S10847; S65690
R;Dickson, L.A.; Ninomiya, Y.; Bernard, M.P.; Pesciotta, D.M.; Parsons, J.; Green, G.; Bi J. Hille: Them. 256, 8407-8415, 1981
A;Title: The exon/intron structure of the 3'-region of the pro-alpha-2(1) collagen gene. A;Reference number: S10847; MUID:81264246; PMID:6267043
                        ;Cross-references: UNIPARC:UP100001712AD; GB:M10581; NID:g211323; PIDN:AAA48637.1; PID:
;Lehrach, H.; Frischauf, A.M.; Hanahan, D.; Wozney, J.; Fuller, F.; Crkvenjakov, R.; Bo
                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 484-505 <LEH>
A;Cross-references: UNIPARC:UP100001712AB; GB:J00837; NID:g4530617; PIDN:AAA51614.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-365 cDIC.
A;Cross-references: UNIPARC:UPI0000177396; EWBL:J00811
A;Note: the authors translated the codon ATA for residue 207 as Asp, AGC for residue 216
                                            RiLehrach, H.; Frischauf, A.M.; Hanahan, D.; Wozney, J.; Fuller, F.; Crkvenjakov, Proc. Natl. Acad. Sci. U.S.A. 75, 5417-5421, 1978
A.fitle: Construction and characterization of a 2.5-kilobase procollagen clone. A;Reference number: ISO171; MUID:79074829; PMID:364479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 IRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YGGQGSDPADVAIQLIFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWID
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C;Genetics: A:Gross-references: UNIPARC:UP1000177397
A;Gene: COLIA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.4%; Score 883; DB 1;
61.4%; Pred. No. 1.4e-68;
iive 44; Mismatches 49;
                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.4%;
Matches 151; Conservative 4
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958 IGPVCF 963
                                                                                                                                     A, Accession: I50171
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                                                                                                                                                           A;Residues: 506-830, Tr, 831-903, Nr, 904-964 <FUL>
A;Residues: 506-830, Tr, 831-903, Nr, 904-964 <FUL>
A;Cross-references: UNIPARC:UF100001712DF; EMBL:V00390; NID:g63248; PIDN:CAA23688.1; PIDR;Avvedimento, E.V.; Vogeli, G.; Yamada, Y.; Maizel, J.V.
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A;Title: Correlation between splicing sites within an intron and their sequence compleme A;Reference number: 150172; MUID:81064671; PMID:6159982
A;Accession: 150172
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A;Molecule type: DNA
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180

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5

Length 964; 49; Indels us-10-677-877a-4.rpr

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A;Molecule type: mENA
A;Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,'
A;Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,'
A;Cross-references: UNIPARC:UPI000016A61C; EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:
A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide B;Seyer, J.M.; Kang, A.H.
B;Seyer, J.M.; Kang, A.H.
A;Chenistry 16, 1158-1164, 1977
A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptides A;Reference number: A90399; MUID:77134724; PMID:557335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galacto
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 186-194 <AILL>
A;Residues: 186-194 <AILL>
A;Cross-references: UNIPARC:UPI0000000B14; GB:S62925; NID:g386425; PIDN:AAD13937.1; PID:S. R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A;Title: Abnormal Type III collagen produced by an exon-17-skipping mutation of the COL3; A;Reference number: S59511; MUID:96067614; PMID:7487954
A;Residues: 302-423 <CHI>A;Residues: 302-423 <CHI>A;Residues: 302-423 <CHI>A;Residues: 302-423 <CHI>A;Residues: 302-431, 1979
A;Cross-references: UNIPPARC:UPI0000173B83; GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:R;Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1979
A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr per A;Reference number: A90414; MUID:79000343; PMID:687591
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A; Mesidues: 399-675, Nv. 677-727 <SRY3>
A; Cross-references: UNIPARC: UP10000173B84
A; Experimental source: liver
R; Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
A; Ticle: Ghen. 266, 5256-5259, 1991
A; Title: G to T transversion at position +5 of a splice donor site causes skipping of the A; Reference number: 155349; MUID: 91161621; PMID: 1672129
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A;Cross-references: UNIPAC:UPI0000004A2; GB:MS9312; NID:g180815; PIDN:AAA52041.1; PID:
R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589; 1980
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R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, P.; Dahl, H.H.M.; Chan,
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A;Reference number: A90438; MUID:80198282; PMID:6246925
                           A; Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen. A; Reference number: S04887; MUID:89386015; PMID:2780304
A; Accession: S04887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: liver A; Oxform to A; Oxform to A; Oxform author submitted corrections to A; Oxform author submitted corrections to A; Oxform author submitted corrections A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H. A; Miller, Ganet. 53, 62-70, 1993 A.A.; J. Hum. Genet. 53, 62-70, 1993 A; Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein
;Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
;Cross-references: UNIPARC:UP10000173B82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Cross-references: UNIPARC:UP10000173B81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,Reference number: I51868; MUID:93304430; PMID:8317500
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A;Residues: 728-895,'A',897-964 <SEY4>
A;Cross-references: UNIPARC:UP10000173B85
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A;Status: translated from GB/EMBL/DDBJ
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A;Reference number: A94562
A;Accession: A94562
Nucleic Acids Res. 17, 6742, 1989
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A, Reference number: S04642
A, Molecule type: mRNA
A, Residues: 1-1196 ALLA>
A, Molecule type: mRNA
A, Reference number: PE0011; MUID:89378752; PMID:2777083
A, Fitle: Cloning and analysis of the 5' portion of the human type-III procollagen gene (A, Residues: 1-176 ALRA)
A, Residues: 1-176 ALRA>
A, Residues: 1-176 ALRA>
A, Residues: UNIPARC: UP1000016A703; GB:M26939; NID:9180813; PIDN:AAA52040.1; PID:
A, Molecule type: DNA
A, Residues: UNIPARC: UP100016A703; GB:M26939; NID:9180813; PIDN:AAA52040.1; PID:
A, Molecule type: mRNA
A, Residues: 1-170 ALLA
A, Residues: 1-
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NyAlternate names: procollagen alpha 1(III) chain
Cispeciaes: Homo sapiens (man)
Cispeciaes: Doubling (man)
Cispeciaes: S05272
A;Reference number: S05272
A;Reference number: S05272
A;Reference number: S05272
A;Reference number: S05272
A;Residues: 1-1240, 'V',1242-1466 <PRC>
A;Residues: 1-1240, 'V',1242-1466 <PRC>
A;Cross-references: UNIFROT:P02461; UNIPARC:UPI000000CDE; EMBL:X14420; NID:g30057; PIDN
B;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A;Title: Structure of cDNA clones coding for the entire prepro-alphal(III) chain of huma
                                              homology
A;Introns: 36/3; 54/3; 90/3; 173/1; 236/3; 317/3
C;Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal hom
C;Keywords: colled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;136-365/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                      Query Match 66.4%; Score 882; DB 2; Length 365; Best Local Similarity 60.2%; Pred. No. 5.1e-69; Matches 148; Conservative 45; Mismatches 53; Indels
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IGPVCF 364
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A; Description: structural component of extracellular fibrous polymer that maintains inters. Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Reywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd F; 1-23/Domain: signal sequence #status predicted <815.
F; 24-153/Domain: amino-terminal propeptide #status predicted <PRO>F; 1-21/Product: collagen alpha 1(III) chain #status predicted <PRO>F; 154-157/Product: collagen alpha 1(III) chain #status predicted <MAT>F; 154-167/Region: amino-terminal nonhelical telopeptide
                                                                                                                                                                                                                                                                                           F;168-1196/Region: helical carbonent (R-G-D) motif F;109-1196/Region: call attachment (R-G-D) motif F;109-11093/Region: call attachment (R-G-D) motif F;1197-11221/Region: carboxyl-terminal nonhelical telopeptide F;1122-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>F;153-154/Cleavage site: pro-Gln (procollagen N-endopeptidase) #status predicted F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte. F;161,1212/Modified site: allysine (Lys) #status predicted
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ne : 23.5753 secs
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Matches 157; Conservative
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Aritie: Molecular cloing and carboxyl-propeptide analysis of human type III procollage A; Reference number: A93551; MUID: 85087944; PMID: 6096827
A; Reference number: A93551; MUID: 85087944; PMID: 6096827
A; Rocession: A93551
A; Rocession: A)3551
A; Residues: 1065-1155, P', 1157-1466 <LOI>A; Residues: 1065-1155, P', 1157-1466 <LOI>B; Remard, B; Remard, B; Remard, B; Remard, B; Remard, B; Brant Biochemistry 25, 1408-1413, 1986
A; Title: Human type III collagen gene expression is coordinately modulated with the type A; Reference number: 152393; MUID: 86187804; PMID: 3754462
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A;Accession: I52393
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
A;Cross-references: UNIPARC:UPI000016A6BS; GB:M13146; NID:g18041S; PIDN:AAAS2003.1; PID:
B;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) Procollagen genes are located on the long arm
A;Reference number: I59025; MUID:85216505; PMID:3858826
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1165-1196 <EMA>
A;Cross-references: UNIPARC:UPI000016A6B6; GB:M11134; NID:G180417; PIDN:AAA52004.1; PID:
B;Chu, M.L.; Well, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
B;Chu, M.L.; Gfo, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III) collagen. F
A;Reference number: A92516; MUID:85157600; PMID:2579949
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A;Cross-references: UNIPARC:UP10000173B89; GB:M10615; GB:M10793; GB:M10794; GB:M10795;
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72

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45;

31; Mismatches

64.7%; Score 859.5; DB 1; Length 1466; 66.5%; Pred. No. 2.6e-66;

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MEDLINE=92157916; PubMed=1787829; Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning C., Olsen A.S., Prockop D.J.; "Completion of the last half of the structure of the human gene for the Pro alpha 1 (I) chain of type I procollagen (COLJA1)."; Matrix 11:375-379(1991).

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NUCLEOFIDE SEQUENCE

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NCBI_TaxID=9606;
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A Ala-Kokko L.,
A Ala-Kokko L.,
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
B Golo005581; C:collagen; IEA.
R GO; GO:0005731; C:coltagen; IEA.
R GO; GO:0005731; C:cytoplasm; IEA.
R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
R GO; GO:0005811; P:phosphate transport; IEA.
R InterPro; IPR0008161; Cilghelix.
R InterPro; IPR0008161; Cilghelix.
R InterPro; IPR0008161; Collagen_C.
R InterPro; IPR000885; Fib_collagen_C.
R InterPro; IPR000805; Fib_collagen_C.
MUCLECTIDE SEQUENCE.
MEDLINE=98107942; PubMed=9443882;
MCDKOO J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J.,
Prockoo D.J.;
"Analysis of the COLIA1 and COLIA2 genes by PCR amplification and
scanning by conformation-sensitive gel electrophoresis identifies only
COLIA1 mutations in 15 patients with osteogenesis imperfecta type I:
identification of common sequences of null-allele mutations.";
Am. J. Hum. Genet. 62:98-110(1998).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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99.6%; Pred. No. 5.1e-111;
ive 1; Mismatches 0; Indels
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Pfam, PF01391; Collagen; 18.
ProDom; PD00000; Clg_helix; 3.
SWART; SM00038; COLFI; 1.
SWART; SM00214; VWC; 1.
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NUCLECTIDE SEQUENCE OF 1-472.

MEDILINES-89025-644; PubMed=3178743;

MEDILINES-89025-644; PubMed=3178743;

Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,

Jaenisch R., Prockup D.J.;

Jaenisch R., Prockup D.J.;

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R GO; GO: 0006817; P: Extracellular matrix structural constituent; IEA.

R GO; GO: 0006817; P: Extracellular matrix structural constituent; IEA.

R GO; GO: 0006817; P: Extracellular matrix structural constituent; IEA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR001007; VWF.C.

R Pfam; PF01391; Collel; 1.

R ProDom; P0002078; Fib_collagen_C; 1.

R ProDom; P0002078; Fib_collagen_C; 1.

R SMART; SM00214; VWC; 1; 1.

R PROSITE; PS011208; VWFC_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
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Dos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.4%; Score 1295; DB 2; Length 1464; 98.4%; Pred. No. 5.2e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1464 AA; 139011 MW; B0581F8D1C89DDE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                NIH MGC Project;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pro alpha 1(1) collagen (Fragment).
                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC036531; AAH36531.1; -; mRNA.
Ensembl; ENSG00000108821; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95ND8 BOVIN PRELIMINARY;
Q95ND8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 98.4
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1460 HVCFL 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 PVCFL 247
                                                                                                                                                                                                                                                                                                                                       rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q95ND8_BO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1343 GQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLQGSNEIEIR 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOGSDPADVAIQLTFLRIMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIBIR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                       TISSUE-Spleen;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohaxa O., Nagase T., Kikuno F.R.;
"None Title.";
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1467 AA; 139196 MW; 976847FDB93B7945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB209597; BAD92834.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-07T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                          annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 98.8%; Score 1313; DB 2; sal Similarity 99.2%; Pred. No. 1.2e-110; 243; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1464 AA
                                                              Collagen alpha 1 chain variant (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha 1 type I collagen, preproprotein.
Name=COLIA1;
           10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 HUMAN
QBN473 HUMAN PRELIMINARY;
QBN473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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SEQUENCE
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1456 PVCFL 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                        Grosse-Hovest L., Brem G.;

A Grosse-Hovest L., Brem G.;

Bubmitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

Bubmitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

Bubl.; AJ312110; CAC38932.1; -; Genomic_DNA.

Bubl.; AJ312111; CAC38932.1; JOINED; Genomic_DNA.

GO; GO:0005581; Cac31agen; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

RO; GO:00052017; F:extracellular matrix structural constituent; IEA.

RO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR008160; COllagen.

R InterPro; IPR008160; COllagen.

R Probom; PR01410; COLFI; 1.

R Probom; PR01408; Fib collagen_C; 1.

SMART; SM00038; COLFI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21023337; PubMed=11147834; DOI=10.1006/abbi.2000.2099; MEDLINE=21023337; PubMed=11147834; DOI=10.1006/abbi.2000.2099; Campbell B.G., Wootton J.A.M., MacLeod J.N., Minor R.R.; Sequence of normal canine COLLAI cDNA and identification of a heterozygous alpha! (I) collagen Gly208Ala mutation in a severe canine osteogenesis imperfecta."; Arch. Biochem. Biophys. 384:37-46(2000).

-! FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                287 AA; 31698 MW; A9122CAEB7DC3DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1290; DB 2;
Pred. No. 1.8e-109;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1460 AA.
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Name=COLIA1;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.1%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 97.1
Matches 238; Conservative
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                                                         NUCLEOTIDE SEQUENCE
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                NCBI_TaxID=9913
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 GQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIBIR 182
-1- SUBUNIT: Trimers of one alpha 2(1) and two alpha 1(1) chains.
-1- PTM: POOLines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-1- DISEASE: Defects in COLIA1 are a cause of osteogenesis imperfects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEGNSRPTYSVTVDGCTSHTGAWGKTV1 EYKTTKSSRLP1 I DVAPLDVGAPDQEFGFDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allysine (By similarity).
5-hydroxylysine (By similarity).
6-hydroxyproline (By similarity).
7-linked (Gal. . ) (By similarity).
8-linked (GlCNAc. . ) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular matrix; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nonhelical region (N-terminal).
Triple-helical region.
Nonhelical region (C-terminal).
Cell attachment site (Potential).
Cell attachment site (Potential).
Pyrrolidone carboxylic acid (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1290; DB 1; Length 1460;
Pred. No. 1.5e-108;
5; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydroxylation; Pyrrolidone carboxylic acid; Repeat; Signal;
Structural protein.
SIGNAL 1 22 By similarity.
                                                                                                                          -!- SIMILARITY: Belongs to the fibrillar collagen family -!- SIMILARITY: Contains 1 VWPC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 G -> A (in OI; severe).
AA; 138762 MW; 58E3674D2B570697 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
N-terminal propeptide.
Collagen alpha 1(I) chai
C-terminal propeptide.
WWFC.
                                                                                                                                                                                                                                                                                                                                          EMBL, AF153062; AAD34619.1; -; mRNA.
Engembl; ENSCAFG0000017018; Canis familiaris.
InterPro; IPR0018161; Clg halix.
InterPro; IPR0018161; Clg halix.
InterPro; IPR001869; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD00007; Clg halix; 2.
ProDom; PD01208; Rib_collagen_C; 1.
PROSITE; PS01208; VWFC_1: 1.
PROSITE; PS50184; VWFC_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 97.1%;
Local Similarity 96.7%;
les 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen; Disease mutation;
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1160
261
1361
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157
1214
1460
92
174
1188
1214
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1160
261
1361
208
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C. Virgin mouse. Taken by biopsy.

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAURDENG R.L., Feingold B.A., Grouse L.H., Derged J.G.,

RIdusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Distribution L., Marusina K.W., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gubaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Manner A., Schein J.B., Jones S.J.M., Marra M.A.,

Roderzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 OGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                    Collal protein (Fragment).
Name=Collal;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Butharia; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB-Manmary tumor, Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.; Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003198; AAH01198.1; -; mRNA. MGI; MGI:88467; Collal. GO; GO:0005615; C:extracellular space; TAS.
                                                                                                                                                                                                                                                                                                                                                                IISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
92.9%; Score 1235; DB 2; Length 5
Best Local Similarity 91.0%; Pred. No. 4.9e-104;
Matches 223; Conservative 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER 1 1
SEQUENCE 589 AA; 58805 MW; 81847495E5E05CEF CRC64;
                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
589 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
Pfam; PF01410; COLFI; 1.
ProDom; PD00007; Clg helix; 1.
ProDom; PD00007; Clg helix; 1.
ProDom; PD002078; Fib_collagen_C; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences."
Q99LL6 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FVB/N;
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                formation in the rat.";

If J. Dent. Res. 78:11-19(1999).

Rell. 28279; CABO0633.1; -; mRNA.

EMBL; 28279; CABO0633.1; -; mRNA.

Ensembl; ENSRNOG000003897; Rattus norvegicus.

RO; GO:0005781; C:collagen; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:000515; F:protein binding; IEA.

RO; GO:000617; P:phosphate transport; IEA.

RO; GO:000617; P:phosphate transport; IEA.

RICEPPO; IRR0008160; Collagen.

RICEPPO; IRR0008160; Collagen.

RICEPPO; IRR001007; VWF_C.

REPODOM; PRO1400; COLFI; 1.

REPODOM; PRO1400; COLFI; 1.

REPODOM; PRO1309; COLFI; 1.

REPODOM; PRO1309; COLFI; 1.

REPODOM; ROMOSS; COLFI; 1.

REPODOM; ROMOSS; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGRYWIDPN
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE-Bone, and Tooth;
MEDLINE=99163824; PubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
"Expression of collagen alphal(I) mRNA variants during tooth and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1453 AA; 137886 MW; E6896BDC19A4A1D8 CRC64;
                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.2%; Score 1238; DB 2; Best Local Similarity 91.0%; Pred. No. 8.5e-104; Matches 223; Conservative 13; Mismatches 9;
                                                                                                                         Created)
                                                                                                                  6 (TrEMBLrel. 01, C
B (TrEMBLrel. 06, I
4 (TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS01208; VWFC_1; 1. PROSITE, PS50184; VWFC_2; 1.
                                                                                                                                                                                           Collagen alphal (Fragment).
                                                                       Q63079 RAT PRELIMINARY;
Q630797
                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1449 PACFV 1453
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                    01-NOV-1996 (
01-JUN-1998 (
01-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
SEQUENCE
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Q99LL6_MOUSE
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464

62

Gaps

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Length 589;

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NUCLEOTIDE SEQUENCE
    Collagen.
SEQUENCE
                                                                       Query Match
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ID Q81049 MG
101-9109 MG
101-1010-20
DT 101-1010-20
DE Procent-20
DE PRO
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TISSUB-MIXE FVB/N;

TISSUB-MARMARY thubMed=12477932; DOI=10.1073/pnas.242603899;

A StraubBerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A StraubBerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhar N.K.,

Alschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhar N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Prange C.,

R Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Wokin T.B., Tonshiyuki S., Carninci P., Prange C.,

R Richards S., Worley K.C., Hale S., Garcina A.M., Gasuka K.A., Gunazato P.H.,

R Richards S., Worley K.C., Hale S., Garcina A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Noticy R. M., Schmutz J., Myers R.M.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

B Scheration and initial analysis of more than 15,000 full-length human
183 AEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 242
                                                                                               525 GEGNSRFTYSTLVDGCTSHTGTWGKTVIEYKTTKTSKLPIIDVAPLDIGAPDQEFGLDIG 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Muridae; Mutinae; Euarchontoglires; Glires; Rodentia; Sciurognathi;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=Mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059281; AAHS9281.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                              PRT; 1225 AA.
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GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR008161; CIg.helix.
InterPro; IPR008160; COliagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
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Pfam; PP01391; Collagen; 14.
Pfam; PP00093; VWC; 1.
ProDom; PD000007; Clg helix; 2.
ProDom; PD002078; Flb_collagen_C; 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01208; VWFC; 1.
PROSITE; PS50184; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                               Q6PCL3;
05-JUL-2004 (TrEMBLrel. 27, C;
05-JUL-2004 (TrEMBLrel. 27, L;
05-JUL-2004 (TrEMBLrel. 27, L;
Collal protein.
Name-Collal;
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CTRAINE-EVBN'N; TISSUE-Colon;

KEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KRIAUSERER, R.L., Ferimoid B.A., Grouse L.H., Derge J.G.,

RIAUSER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

M Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reperation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                            DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN 1040
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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                                                                92.9%; Score 1235; DB 2; Length 1225;
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1225 AA; 117860 MW; B6B86CBB4457F4D9 CRC64;
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01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
10-MNY-2005 (TrEMBLrel. 20, Last annotation update)
Procollagen, type I, alpha 1.
Name-Collal; ORFNames=RP23-112C19.9-001;
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                                                                                                                                               10;
                                                                                                     Pred. No. 1.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1453 AA
                                                                                                             Best Local Similarity 91.0%; γreα. νο. 1..υσ·
Matches 223; Conservative 12; Mismatches
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STRAIN=FVB/N; TISSUE=Colon;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q810J9 MOUSE PRELIMINARY;
Q810J9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae; Murinae; Mus
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                                                                                                     Local Similarity
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Construction and characterization of cDNA clones encoding the 5' end
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes; Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE OF 1-153.
MEDLINE=88056316; PubMed=3678834; DOI=10.1016/0378-1119(87)90159-4;
Finer M.H., Boedtker H., Doty P.;
                                                                                                                                                                                             ö
                                                                                                                                                                                92.9%; Score 1235; DB 2; Length 1453; 91.0%; Pred. No. 1.6e-103; ive 12; Mismatches 10; Indels 0.
                                                                                                                                                                     1453 AA; 138032 MW; 0B7F06BBB9A1D5EA CRC64;
                              Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
      Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
                                 1011-1986 (Rel. 01, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                PRT; 1453 AA.
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                   NUCLEOTIDE SEQUENCE
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1449 PACFV 1453
                                                                                                                                                                                        Similarity
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                                                                                                                                                                                            Matches 223;
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                                                                                                                                                                Collagen.
SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=72243016; PubMed=5047697;

Eyre D.R., Glimcher M.J.;

"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";

Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 152-1187.
MEDLINE-82231995; PubMed-7093229;
Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chicken pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino acid sequence of chick skin collagen alpha 1(1)-CB8 and the complete primary structure of the helical portion of the chick skin collagen alpha 1(1) chain."; collagen alpha 1(1) chain."; alsochemistry 21:2048-2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE OF 1311-1453.
MEDLINE=80134546; PubMed=6987088; DOI=10.1016/0014-5793(80)80761-7;
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MICLIONE 31160715, PubMed=6927845;

Fuller F., Boedtker H.,

"Sequence determination and analysis of the 3' region of chicken prasequence determination and analysis of the 3' region of chicken prasequence determination and analysis of the 3' region of chicken prasequence determination and analysis of the 3' region of chicken praints alpha 1(1) and provabla 2 (1) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences.";

Biochemistry 20:996-1006(1981).
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-!- PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxypro proline in position X.

-!- SIMILARITY: Belongs to the fibrillar collagen family.
-!- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                 MEDLINE-88007542; PubMed=2820966; Finer M.H., Abo S., Gerstenfeld L.C., Boedtker H., Doty P.; "Unmual DNA sequences located within the promoter region and first intron of the chicken pro-alpha 1(I) collagen gene."; J. Biol. Chem. 262:13323-13332(1987).
of the chicken pro alpha 1(I) collagen mRNA.";
Gene 56:71-78(1987).
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EMBL; W17839; AAA48704.1; O'DINED; Genomic_DNA.
EMBL; VOOAQ1; CAA23695.1; -; mRNA.
EMBL; M10571; AAA48671.1; ALT_SEQ; mRNA.
EMBL; M17607; AAA48672.1; -; mRNA.
PIR; A27179; A27179.
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InterPro; IPR008160; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .) (By similarity).
                                                                                                                                                                                           Collagen, Direct protein sequencing, Extracellular matrix;
Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-linked (Gal. . .) (By similarity)
N-linked (GlcNAc. . .) (By similari
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                                                                                                                                                                                                                                                                                                                                                                                                                    Allysine (By similarity).
5-hydroxylysine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-hydroxylygine (Potential).
Hydroxyproline (Potential).
5-hydroxylygine (Potential).
3-hydroxyproline.
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Collagen alpha 1(I) chain.
C-terminal propeptide.
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                      Pfam, PF00093; VWC; 1.
Probom, PD000007; Clg_helix; 2.
Probom, PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00141; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
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Li S.W., Khillan J., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.2%;
Pfam; PF01391; Collagen; 18
                                                                                                                                                                                                                                           Signal; Structural protein
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Matches 218; Conservative
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MEDIJUE=86137403; PubMed=3841523; DOI=10.1016/0378-1119(85)90329-4;
French B.T., Lee W.-H., Maul G.G.;
"Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                       "Genomic sequence of mouse COLIA1 encoding the collagen propeptides."; Biochim. Biophys. Acta 1216:469-474(1993).
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"DNA methylation represses the murine alpha 1(I) collagen promoter by
"The complete cDNA coding sequence for the mouse pro alpha 1(I) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84170331; PubMed-6324198; Harbers K., Kuehn M., Delius H., Jaenisch R.; Insertion of retrovirus into the first intron of alphal(I) collagen gene leads to embryonic lethal mutation in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
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MEDLINE-94092741; PubMed-8268229; DOI=10.1016/0167-4781(93)90016-7;
Fenton S.P., Lamande S.R., Hannagan M., Stacey A., Jaenisch R.,
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Momson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse pro alpha 1(1) procollagen gene
evidence for insertions or deletions in gene coding sequences.";
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"Specific hybridization probes for mouse type I, II, III and IX
"Specific hybridization probes for mouse type I, II, III and IX
collagen mRNAs.",

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elochiam. Biophys. Acta 1089:241-243(1991).

elochiam. Biophys. Toma III and two alpha I(I) chains.

elochiam. Fight Specific Try: Forma the fibrils of tendon, ligaments an bones. In bones the fibrils are mineralized with calcium
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MEDLINE-88124276; PubMed-3340560;
MOOBLEAIDER K., Harbers K.,
"Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the the 3'-untranslated region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83141374; PubMed-6298597;
Monson J.M., Friedman J., McCarthy B.J.;
"DMA sequence analysis of a mouse pro alpha 1 (I) gevidence for a mouse B1 element within the gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an indirect mechanism.";
Mol. Cell. Biol. 14:5950-5960(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6; TISSUE=Liver;
MEDLINE=94344105; PubMed=8065328;
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                                          of type I procollagen.";
Matrix Biol. 14:593-595(1995)
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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EMBL; 867920; AAA8891211; -; GENOMIC_DNA.

EMBL; X54876; CAA3866711; ALT SEQ; GENOMIC_DNA.

EMBL; X54876; CAA3866711; ALT SEQ; GENOMIC_DNA.

EMBL; M14423; AAA37333.1; -; GENOMIC_DNA.

EMBL; M03029; AAA37332.1; -; GENOMIC_DNA.

EMBL; K03031; AAA37332.1; -; GENOMIC_DNA.

EMBL; K03031; AAA37332.1; JOINED; GENOMIC_DNA.

EMBL; K03034; AAA37332.1; -; GENOMIC_DNA.

EMBL; K03034; AAA37332.1; -; GENOMIC_DNA.

EMBL; K03034; AAA37332.1; -; GENOMIC_DNA.

EMBL; K155981; CAA43964.1; -; GENOMIC_DNA.

EMBL; EMBL; K155981; FIB. CALIBGEN. 18.

EMBL; EMBL; EMBLY EMBL; TAETHY; GLIAGEN. 18.

EMBL; EMBL; EMBL; EMBL; TAETHY; EMBL; TAETHY; TAETHY; TAETHY IN THE 
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Triple-helical region (C-terminal).
Cell attachment site (Potential).
Cell attachment site (Potential).
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MW; 3B802E535DF81808 CRC64;
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Collagen alpha 1(1) chain.
C-terminal propeptide.
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Gaps

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Indels

91.6%; Score 1218; DB 1; 89.8%; Pred. No. 5.7e-102; tive 12; Mismatches 13;

Best Local Similarity 89.6 Matches 220; Conservative

Query Match

Length 1453;

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1269 QGCNLDAIKVYCNWETGQTCVFPIQPSVPQKNWYISPNPKEKKHVWFGESMTDGFPFEYG 1328
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                                                                                                                              123 GQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR 182
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, U03419; AAA03475.1; -; mRNA.
MG1; MG1:88467; Colla1.
GO; GO:0005615; C:extracellular space; TAS.
Interpro; IPRO08160; Collagen.
Interpro; IPRO0886; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
Probom; PD002078; Fib_collagen_C.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
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SEQÜENCE 325 AA; 35229 MW; A5A21E74DFDE3EF1 CRC64;
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Last annotation update)
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Name=Colla1;
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01-NOV-1996 (TEMBLrel. 01, Last seq
01-OCT-2003 (TEMBLrel. 25, Last ann
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060785 MOUSE
D 060785 MOUSE PRELIMINARY;
AC 060785;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 218; Conserv;
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RESULT 14

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1205 DANVWRDRDHEVDSTLKSLSKQIENIQSPEGTRKNPARTCRDLKMCHSDWKSGEYWIDPN 1264
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A Klein S., Gerbard D.S.;

Bubmitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

Braembl.; BCO82718; AAM82718.1; -; mRNA.

Rasembl.; ENSXETG0000003374; Xenopus tropicalis.

RGO; GO:0005531; C:collagen; IEA.

RGO; GO:0005373; C:cytoplasm; IEA.

RGO; GO:0005373; C:cytoplasm; IEA.

RGO; GO:0005371; P:phosphate transport; IEA.

RICEPTO; IPR0008161; Clq helix.

RICEPTO; IPR001007; VWF_C.

RICEPTO; IPR0100107; VWF_C.

REAM; PP01341; Collagen; 18.

REAM; PP00134; Collagen; 18.

REAM; PP00003; VWC; 1.

REAM; PP00003; VWC; 1.

REAM; PP00003; VWC; 1.

REAM; PP00003; VWC; 1.

REAM; PP00007; Clq_helix; 4.

REAM; PP00007; Clq_helix; 4.
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                                                                                                                                    Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00038; COLFI; 1.

SMART; SM00214; VWC; 1.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS01208; VWFC_2; 1.

Collagen; Hypothetical protein.

SEQUENCE 1449 AA; 137539 MW; 456639B1687A3B4B CRC64;
                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotheical LOC496414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
1449 AA
                                                                                                                                                                                             Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
Q640B2_XENTR PRELIMINARY;
                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                          NCLEGOTIBE SEQUENCE.

NUCLEGOTIBE SEQUENCE.

X MEDLINE-99407244; PubMed=10474166;

X DOI=10.1002/(SICI)1097-0177(199909) 216:1<59::AID-DVDY8>3.3.CO;2-2;

Agahina K., Obara M., Yoshizato K.;

Asahina K., Obara M., Yoshizato K.;

Bereveloyment of the blastema of regenerating newt limb.";

Dev. Dyn. 216:59-71(1999).

EMBL; AB015438; BAA36973.1; -; mRNA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RITHEFPO: IPR000885; Pib_collagen_C.

RITHEFPO: IPR000885; Pib_collagen_C.

REAMRT; SM002078; Fib_collagen_C; I.

RODOM; PD0002078; Fib_collagen_C; I.

RODOM; PD0002078; Fib_collagen_C; I.

RODOM; ROMOSSE COLFI; I.
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                                                                                                                                                                                                                                          Alpha 1 type I collagen.
Cynops pyrrhogaeter (Japanese common newt).
Ebkaryota, Metazoa; Chodata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
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87.8%; Pred. No. 8.9e-101;
ive 19; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                           PRT; 1450 AA.
                                                                                                                                                                                   Created)
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PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10,
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Matches 215; Conservative 1
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Q9YIB4;
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243 PVCFL 247
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²⁴³ PVCFL 247 ||||: 1445 PVCFV 1449

Search completed: April 26, 2006, 16:19:22 Job time : 134.566 secs

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Sequence 14, Appli
Sequence 9, Appli
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Sequence 18, Appl
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1329
1 RSDANVVRDRDLEVDTTLKS......LDVGAPDQEFGFDVGPVCFL 247
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/laa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
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US-09-585-887-9
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US-09-331-347C-21
US-09-50-811-18
US-09-50-611-18
US-09-50-611-18
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US-09-50-811-18
US-09-50-811-18
US-09-50-811-12
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2 US-09-919-497-56 2 US-09-795-061-4 5 US-09-949-002-405 1 US-09-949-002-492 1 US-09-949-002-492 2 US-09-795-061-2 2 US-09-104-047-2717 2 US-09-104-047-2717 2 US-09-104-047-2717 2 US-09-104-104-104 1 US-08-553-497A-22 1 US-08-553-497A-24 1 US-08-553-497A-24	ALIGNMENTS	SEULT 1   1   1   1   1   1   1   1   1   1	5/09585887
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3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		RESULT 1 US-09-029- 1 Sequence 1 Patent I 1 GENERAL I 2 APPLICT I 2 FILLE R 2 FILLE R 3 CURRENY 3 CURRENY 4 CURRENY 5 SOFTWAR 6 SOFTWAR 6 COTHER 7	US-09-5 ; Seque ; Pater
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j Patent No. 6428978
j GENERAL INFORMATION:
j GENERAL INFORMATION:
j APPLICANT: Chang, Robert
j APPLICANT: Chang, Robert
j APPLICANT: Hitzeman, Ronald A.
j APPLICANT: Chisholm, George
j TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
j TITLE OF INVENTION: CELLS
j FILE REFERENCE: 225002030400
j CURRENT APPLICATION NUMBER: US/09/289,578
j FILE APPLICATION NUMBER: 60/084,828
j PRIOR APPLICATION NUMBER: 60/084,828
j NUMBER OF SEQ ID NOS: 11
j SOFTWARE: PatentIn Ver. 2.0
j SEQ ID NO 9
j TANGTH. 100 9
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            APPLICANT: Olsen, David R
APPLICANT: Clang, Robert
APPLICANT: Clang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: CVLL. ENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CVLL. ENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CVLL. ENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
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TITLE OF INVENTION: CVLL. ENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CVLL. ENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION NUMBER: 09/289,578
PRIOR PLILING DATE: 1998-06-09
PRIOR PLILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN VOY: 2.0
SEQ ID NO 9
LENGTH: 1461
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99.6%; Pred. No. 1.1e-133;
iive 1; Mismatches 0;
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Best Local Similarity 99.6
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-585-887-9
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Met
TITLE OF INVENTION: obtaining Such and Their Uses
TITLE REPERENCE: 1149-3
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT APPLICATION NUMBER: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1464
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     Length 1461;
                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1317; DB 2;
Pred. No. 1.1e-133;
1; Mismatches 0;
99.1%; Score 1317; DB 2;
99.6%; Pred. No. 1.1e-133;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/09331347C
Patent No. 6617431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.1%;
  Query Match
Best Local Similarity 99.6
Matches 244; Conservative
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Best Local Similarity 99.6
Matches 244; Conservative
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CORGANISM: Homo sapiens
US-09-331-347C-21
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                                Patent No. 6110689
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEB: Darby & Darby PC
STREET: 805 Third Avenue
CITT: New York
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1276 RAEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDV 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1299.5; DB 2
Pred. No. 7.9e-132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIE, Adda C
REGISTRATION NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                   ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 Sequence 18, Application US/08963825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLEAGE: COLLAGEN ALPHA 1 (I)
US-08-963-825-18
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.8
Best Local Similarity 98.8
Matches 243; Conservative
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US-08-963-825-18
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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116 GGGGSDPADVAIQLTFLEREMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEI 1275 1096 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGXRKNPARTCRDLKMCHSDWKSGEYWIDPN 1155 122 GGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQOTGNLKKALLLKGSNEIEI 3 DANVVRDRDLBVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN 63 QGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDK-RHVWFGESMTDGFQFEY 182 RAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDV 1; Score 1299.5; DB 2; Length 1341; Pred. No. 7.9e-132; 0; Mismatches 2; Indels 1; SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE: CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERRINCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-27-7700
TELEFAX: 212-753-6237
TELEFAX: 212-753-637
TELEFXX: 212-753-637
TELEFXX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS IMMEDIATE SOURCE: CLONE: COLLAGEN ALPHA 1 (I) Query Match
Best Local Similarity 98.8%;
Matches 243; Conservative LENGTH: 1341 amino acids MEDIUM TYPE: Floppy disk ORGANISM: Homo sapiens TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: COMPUTER READABLE FORM: TYPE: amino acid US-09-500-811-18

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GENERAL INFORMATION:
APPLICANT: Qviet, Per
APPLICANT: Qviet, Per
APPLICANT: Qviet, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out t
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
1276 RAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDV 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1096 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGXRKNPARTCRDLKMCHSDWKSGEYWIDPN 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1299.5; DB 2
Pred. No. 7.9e-132;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
RESTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08
                                                                                                                                                                                                                                         Sequence 18, Application US/09548608
Patent No. 6355442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) IMMEDIATE SOURCE:
) CLONE: COLLAGEN ALPHA 1 (I)
US-09-548-608-18
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TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.8%;
Best Local Similarity 98.8%;
Matches 243; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                     1336 ĠPVĊFĽ 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                           242 GPVCFL 247
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10022
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US-09-548-608-18
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the Presence of
of
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                                                                                                                                                        Sequence 18, Application US/09570573

Sequence 18, Application US/09570573

Patent No. 6342361

GENERAL INFORMATION

APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carr

TITLE OF INVENTION: Disorders Associated with the Metabolism of

TITLE OF INVENTION: Disorders Associated with the Metabolism of

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby PC

STREET: 805 Third Avenue

CITY: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.8%; Score 1299.5; DB 3
Best Local Similarity 98.8%; Pred. No. 7.9e-132.
Matches 243; Conservative 0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                    GPVCFL 1341
     GPVCFL 247
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                                                                                                                        RESULT 7
US-09-570-573-18
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119 FEYGGQGSDPADVAIQLTFIRIMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.9%; Score 982.5; DB 2; Best Local Similarity 69.1%; Pred. No. 2.7e-97; Matches 172; Conservative 36; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4305/08701
                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09500811
Patent No. 6323314
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for As
TITLE OF INVENTION: In Body Fluids,
TITLE OF INVENTION: Disorders Assoc
TITLE OF INVENTION: Disorders Assoc
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFRENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLLAGEN -ALPHA 1 (II)
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ET: 805 Third Avenue
: New York
E: New York
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                     239 FDVGPVCFL 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-500-811-20
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Patent No. 6110689

GENERAL INFORMATION:
APPLICANT: Oviet, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1216 GGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEI 1275
                                                                    1276 RAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDV 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPTCATION: 436
PRIOR APPLICATION DATA.
PPLICATION NUMBER: US/08/187,319
PILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIA, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 236687
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.99
Best Local Similarity 69.15
Matches 172; Conservative
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                                                                                                                                                                  1336 GPVĊFĽ 1341
                                                                                                                            GPVCFL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10022
                                                                                                                                                                                                                              RESULT 9
US-08-963-825-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Ne
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                                            182
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Carrying Out the
the Presence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSD--ANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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A Method for Assaying Collagen Fragments
in Body Fluids, A Test Kit and Means for Carrying Out
Method and Use of the Method to Diagnose the Presence
Disorders Associated with the Metabolism of
59 IDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 118
                                                                                                                                                                                                        119 FEYGGQGSDPADVAIQLTFLRIMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 178
                                                                                                                                                                                                                                                                                                                          179 IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1418;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 982.5; DB 2;
Pred. No. 2.7e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09548608
Patent No. 6355442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,714
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TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.9%;
69.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 1418 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Goode, Martin
TITLE OF INVENTION: in F
TITLE OF INVENTION: Disc
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||||||
1410 VDIGPVCFL 1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                               239 FDVGPVCFL 247
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10022
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Sequence 20, Application US/09570573
Sequence 20, Application US/09570573
Sequence 20, Application US/09570573
Sequence 20, All 2
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                                         179 IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 238
        IDPNOGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 118
                                                                                                                       FEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 982.5; DB 2;
Pred. No. 2.7e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.9%; Score 982.5; D
Best Local Similarity 69.1%; Pred. No. 2.7e-
Matches 172; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 6090riah, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFANK: 212-527-7700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEB: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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1410 VDIGPVCFL 1418
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US-09-570-573-20
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1231 IDPNQGCTLDAMKVFCNMETGETCVYPNPANVPKKNWWSSKS-KEKKHIWFGETINGGFH 1289
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                                                                                                                          Gaps
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E
                                                         Length 1418;
                                                                                                                      Indels
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COMPUTE: TEXABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,650
FLING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/316,650
FLING DATE: 30-SEP-1994
ATTONENY/AGENT INFORMATION:
NAME: PARKENCE JOSCH 1994
ATTONENY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
TELEROMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION 
                                                         Query Match 73.6%; Score 977.5; DB 2; Best Local Similarity 68.7%; Pred. No. 9.4e-97; Matches 171; Conservative 36; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Roseler, Blake J.
APPLICANT: Goldstein, Steven A.
APPLICANT: Lin, Wushan
ITILE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: FOR STIMULATING BONE CELLS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Arnold, White & Durkee P.O. Box 4433
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TELLEX: 79-0294
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
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CITY: Houston
STATE: Texas
COUNTRY: USA
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US-09-010-999-1
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; Sequence 1, Application US/09010999
; Patent No. 6132976
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Billinghurat, R. C.
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Poley & Lardher
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Machington
                                                             1 RSD--ANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
38; Indels
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ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,999

FILING DATE: 22-AN-1998

CLASSIFICATION NUMBER: US 08/448,501

FILING DATE: 17-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/984,123

FILING DATE: 04-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 20,768

REFERENCE/DOCKET NUMBER: 29,768
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human Type II Collagen
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
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(202) 672-5399
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1410 vĎIGPVĊFĽ 1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
Matches 172;
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                                                                                                                                                                                                                                                                                                                                      185 GNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVGPV 244
                                                                                                              5 NVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQG
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS AND COMPOSITIONS FOR STIMULATING BONE CELLS
                                                                           ;
                                    72.8%; Score 967.5; DB 1; Length 1442; 68.3%; Pred. No. 1.2e-95; ive 39; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9S/02251
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMICOO9P--
TELEPOMMUNICATION INFORMATION:
TELEFAX: (713) 789-2679
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
PCT-US95-0251-12
i Gequence 12, Application PC/TUS9502251
i GENERAL INFORMATION:
APPLICANT:
ITILE OF INVENTION: METHODS AND COMPOS;
ITILE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FBB-1994
CLASSIFICATION:
                                                    Best Local Similarity 68.39
Matches 166; Conservative
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US-08-316-650-12
                                    Query Match
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1320 NLAPNTANVQMTFLRLLSTEGSQNITYHCKNSIAYLDEAAGNLKKALLIQGSNDVEMRAE 1379
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                                                                                                                                                                 5 NVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQG
                                                                                                                     1;
                                                                         Length 1442;
                                                                                                                  Indels
                                                                    Query Match 72.8%; Score 967.5; DB 4; Best Local Similarity 68.3%; Pred. No. 1.2e-95; Matches 166; Conservative 39; Mismatches 37;
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Job time : 19.5914 secs
MOLECULE TYPE: peptide
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PCT-US95-02251-12
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884, App 243, App 24, Appl 24, Appl 2, Appli 6, Appli 6, Appli 6367, Ap 26, Appl 70, Appl 70, Appl 717, Appl 717, Appl 717, Appl 717, Appl 717, Appl 717, Appl 718, Appl 719, Ap

Sequence Sequence :

Sequence Seq

Run

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US-10-358-024-1

US-10-788-792-150

US-09-925-301-884-

US-10-921-265-243

US-10-058-124-18

US-10-402-099-2

US-10-402-089-8

US-10-402-072A-2

US-10-402-073A-8

US-10-402-072A-2

US-10-402-072A-2

US-10-402-072A-2

US-10-402-072A-2

US-10-402-072A-2
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US-10-366-125-17
US-10-058-124-20
US-10-468-091-5
US-10-756-149-4739
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VGPVCFL 247
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US-10-677-877A-4
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Sequence 159, App
Sequence 2, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 79, Appl
Sequence 261, App
Sequence 1289, Ap
Sequence 157, App
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6, Appli
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                                                                        April 26, 2006, 16:17:23 ; Search time 50.905 Seconds (without alignments) 2027.381 Million cell updates/sec
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                                                                                                                                           1 RSDANVVRDRDLEVDTTLKS......LDVGAPDQEFGFDVGPVCFL 247
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Sequence 8,
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Sequence 81
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-677-877A-16
US-10-677-877A-18
US-10-677-877A-12
US-10-133-794-81
US-10-133-794-81
US-10-677-877A-10
US-10-677-877A-10
US-10-677-877A-14
US-10-677-877A-14
US-10-677-877A-14
US-10-677-877A-14
US-10-17-293-65
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Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Result ě

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Sequence 4, Application US/10677877A

Sequence 4, Application US/1067787A

Publication No. US20050202537A1

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: Methods and composition for producing secreted trimeric

TITLE OF INVENTION: receptor analogs and biologically active fusion proteins

TITLE OF INVENTION: VANDER: US/10/677,877A

CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 4

LENGTH: 247
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Sequence 16, Application US/10677877A

Publication No. US20050202537A1

GRNERAL INFORMATION:

APPLICANT: Liang, Peng; GenHunter Corporation

TITLE OF INVENTION: Methods and composition for producing secreted trimeric
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99.3%; Score 1320; DB 4; Length 258;
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; OTHER INFORMATION: Translation of SEQ ID NO:80
US-10-139-794-81
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Best Local Similarity 100.0
Matches 246; Conservative
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ORGANISM: Homo Sapiens
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US-10-677-877A-12
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US-10-139-794-81
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FILE REFERENCE: 03-052-PL CURRENT APPLICATION: receptor analogs and biologically active fusion proteins CURRENT APPLICATION NUMBER: US/10/677,877A CURRENT FILING DATE: 2003-10-02 NUMBER OF SEQ ID NOS: 16 SEQ ID NO 16 TENDER OF SEQ ID NOS: 16
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Sequence 8, Application US/205202637A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
FILE REFERENCE: 03-052-PL

CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16
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ORGANISM: Homo sapiens
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US-10-677-877A-8
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Sequence 81, Application US/10139794
; Publication No. US20030232421A1
; Sequence 81, Application No. US20030232421A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
THEORMATICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun Luo
TITLE OF INVENTON: Protein-Protein Interactions In Adipocyte Cells (3)
FILE REFERENCE: B4883A
CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/10/139,794
; CURRENT FILING DATE: 2001-05-04
; PRIOR PLILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 2930
; SCFTWARE: Patentin version 3.1
; SEQ ID NO 81
Sequence 12, Application US/10677877A

Publication No. US2005020537A1

GENERAL INFORMATION:

APPLICANT: Liang, Peng; GenHunter Corporation

APPLICANT: Liang, Peng; GenHunter Corporation

TITLE OF INVENTION: Methods and composition for producing secreted trimeric

TITLE OF INVENTION: receptor analogs and biologically active fusion proteins

FILE REFERENCE: 03-052-PL

CORRENT APPLICATION NUMBER: US/10/677,877A

CURRENT APPLICATION NUMBER: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 12
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ORGANISM: Homo sapiens
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Publication No. US20050202537A1

GENERAL INFORMATION:

APPLICANT: Liang, Peng; GenHunter Corporation

TITLE OF INVENTION: methods and composition for producing secreted trimeric

TITLE OF INVENTION: receptor analogs and biologically active fusion proteins

FILE REFERENCE: 03-052-PL

CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT APPLICATION DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16

SEQ ID NO
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                0; Indels
100.0%; Pred. No. 7.7e-125; ive 0; Mismatches 0;
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US-10-677-877A-10
S-20-ence 10, Application US/10677877A
Publication No. US20050202537A1
GENERAL INFORMATION:
APPLICANT: Liang, Peng; GenHunter Corporation
Best Local Similarity 100.
Matches 245; Conservative
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TITLE OF INVENTION: Methods and composition for producing secreted trimeric TITLE OF INVENTION: receptor analogs and biologically active fusion proteins FILE REPERBURG: 03-052-PL CURRENT APPLICATION NUMBER: US/10/677,877A CURRENT FILING DATE: 2003-10-02 SEQ ID NO 10 LENGTH: 566
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Matches 245; Conservative
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; ORGANISM: Homo sapiens US-10-060-036-159
ORGANISM: Homo sapiens
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US-10-060-036-159
     ; ORGANISM: noun
US-09-918-715-261
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Publication No. US20050202337A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and composition for producing secreted trimeric
TITLE OF INVENTION: receptor analogs and biologically active fusion proteins
TITLE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/677,877A

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 16
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635 AEGNSRFTYSVTVDGCTSHTGAMGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVG 694
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Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Brad &C. Croix

APPLICANT: Brat Vogelstein

APPLICANT: Renneth Kinzler

TILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: 08/09/918,715

CURRENT PILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR PLICATION NUMBER: 50/224,360

PRIOR PLICATION NUMBER: 50/224,360

PRIOR PLICATION NUMBER: 50/224,360

PRIOR PLICATION NUMBER: 60/224,360

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                                                  243 PVCFL 247
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US-09-918-715-261
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US-10-677-877A-6
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APPLICANT: Kalos, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jang, Yuqiu H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
CURRENT APPLICATION WUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 159
LENGTH: 1464
TWODE: DOWN
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                                                        Indels
Query Match 99.3%; Score 1320; DB 3; L
Best Local Similarity 100.0%; Pred. No. 8.4e-124;
Matches 245; Conservative 0; Mismatches 0;
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Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
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TYPE: PRT
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APPLICANT:
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APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Galt, Karen
APPLICANT: Galt, Karen
APPLICANT: Ganavarapu, Manjula
APPLICANT: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
ITILE OF INVENTION: OF CERVICAL CANCER
FILE OF INVENTION NUMBER: US 60/298,159
RIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FabltScy for Windows Version 4.0
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Publication No. US20030105050A1
GENERAL INFORMATION:
APPLICANT: Beri, Rajinder
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
FILE REPERENCE: 06275-224US1
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 2002-06-10
                                                                                                                                    ; Sequence 36, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Zhao, Xumei
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1460 PVCFL 1464
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APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Pustai, Lajos
APPLICANT: Pustai, Lajos
APPLICANT: Pustai, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
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CURRENT FILING DATE: 2002-06-21
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PRIOR FILING DATE: 2001-06-21
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PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
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PRIOR PEDIACHTON NUMBER: US 60/301,572
PRIOR FILLING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
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Publication No. US20030124128A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-12-12
PRIOR PELLING DATE: 2000-12-15
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 4.0
SEQ ID NO 2
LENGTH: 1464
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Kamatkar, Shubhangi
Mertens, Maureen
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Hoersch, Sebastian
Monahan, John
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Wang, Youzhen
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US-10-149-352-2
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GENERAL INCHARATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Monahani, John E.

APPLICANT: Monahani, John E.

APPLICANT: Monahani, John E.

APPLICANT: Monahani, John E.

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION NUMBER: US 60/339,971

PRIOR FILING DATE: 2002-11-21

PRIOR FILING DATE: 2001-12-10

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 228

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PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 1464
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-177-293-65
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US-10-301-822-28
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3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
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                                                                                                                                                      April 26, 2006, 16:18:13; Search time 9.73835 Seconds (without alignments) 1153.484 Million cell updates/sec
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1: /SIDS5/ptodata/2/pubpaa/US08_NEW PUB.pep:*
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3: /SIDS5/ptodata/2/pubpaa/US07_NEW PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-784-004-918

US-10-784-004-918

US-11-202-057-3

US-11-202-057-3

US-11-202-057-3

US-11-202-057-3

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US-11-186-284-31

US-11-051-720-1447

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Listing first 45 summaries
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Sequence 331, Application US/10501035

Publication No. US20060046249A1

GENERAL INFORMATION:

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TITLE OF INVENTION:

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APPLICATION NUMBER: US/10/501,035

CURRENT APPLICATION NUMBER: US/10/501,035

PRIOR APPLICATION NUMBER: US 60/350,061

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Sequence 915, App
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Sequence 913, App
Sequence 131, App
Sequence 1181, App
Sequence 1381, App
Sequence 1381, App
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                                      US-110-995-561-913
US-11-124-5168A-329
US-11-074-518A-329
US-11-054-515-1381
US-11-054-515-1381
US-11-054-515-1001
US-11-054-515-1001
US-11-054-515-1688
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ORGANISM: Homo sapiens
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APPLICANT: Gaillemette, Tracy L.
APPLICANT: Gaillemette, Tracy L.
APPLICANT: Gaillemette, Tracy L.
APPLICANT: Samatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Milbodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, THERARY OF COLON CANCER
TITLE OF INVENTION: THERARY OF COLON CANCER
TITLE OF INVENTION: THERARY OF COLON CANCER
TITLE OF INVENTION: THERARY OF COLON CANCER
TITLE APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-10-20
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
PRIOR FILING DATE: 2020-05-20
NUMBER OF SEQ ID NOS: 228
TENGTH: 1464
TTYPE: PRT
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; Sequence 2, Application US/11021603
; Publication No. US20060003954A1
; GENERAL INFORMATION:
   APPLICANT: Beri, Rajinder
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
; FILE REPERENCE: 06275-254US1
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/11/199,352
; PRIOR PILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/GB00/04741
; PRIOR PILING DATE: 2000-12-12
                      ; Sequence 28, Application US/11186284; Publication No. US20050266493A1; GENERAL INFORMATION;
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1220 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN 1279
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APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE KEFERENES: 785-CLPACN
CURRENT PRILING DATE: 2004-11-29
RIOR APPLICATION NUMBER: 10/291, 265
PRIOR PILING DATE: 2004-11-29
PRIOR PILING DATE: 2001-08
PRIOR PILING DATE: 2001-08-05
PRIOR PLING DATE: 2000-08-05
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-77
PRIOR PLING DATE: 2000-01-77
PRIOR PLING DATE: 2000-01-77
PRIOR PLING DATE: 2000-01-77
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-015
NUMBER OF SEQ ID NOS: 944
SOFTWARE: PASHERO for Windows Version 3.0
SERGID NO 243
LENGTH: 1464
PRIOR APPLICATION NUMBER: GB 9929487.8
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 4.0
SEQ ID NO 2
ILBNGTH: 1464
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 243, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
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APPLICANT: Liu, Chenghua
APPLICANT: Asuudi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
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1389 GEGNSRFTYSTLVDGCTSHTGTWGKTVIEYKTTKTSRLPIIDVAPLDIGAPDQEFGMDIG 1448
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US-10-784-004-434
| US-10-784-004-434
| Sequence 434, Application US/10784004
| Publication No. US20060084066A1
| GENERAL INFORMATION:
| APPLICANT: Biogen Idec
| TITLE OF INVENTION: Surrogate Markers of Pain FILE REFERENCE: 08201.6029-00000
| CURRENT APPLICATION NUMBER: US/10/784,004
| CURRENT FILING DATE: 2004-02-20
| NUMBER OF SEQ ID NOS: 1251
| SOFTWARE: Patentin version 3.2
| LENGTH: 1453
| TYPE: PRT
                                                                                                     Sequence 344, Application US/10784004
Publication No. US20060084066A1
GENERAL INFORMATION:
APPLICANT: Blogen Idec
TITLE OF INVENTION:
FILE REPERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
SEQ ID NO 344
ILENGTH: 1453
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1463 PVCFL 1467
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US-10-784-004-434
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, W. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1096
LENGTH: 1467
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                                                                      Query Match 98.8%; Score 1313; DB 7; Length 1464; Best Local Similarity 99.2%; Pred. No. 1.2e-115; Matches 243; Conservative 2; Mismatches 0; Indels 0
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Best Local Similarity 99.2
Matches 243; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-243
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US-10-821-234-1096
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; TYPE: PRT
; ORGANISM: rat
US-10-784-004-950
LENGTH: 1453
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                                                           123 GQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIR 182
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OGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG 122
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93.2%; Score 1238; DB 6;
Best Local Similarity 91.0%; Pred. No. 1.4e-108;
Matches 223; Conservative 13; Mismatches 9;
                                                                                                                                                                                                                                                                               Sequence 918, Application US/10784004

Publication No. US20060084066A1

GENERAL INFORMATION:

TITLE OF INVENTION: Surrogate Markers of Pain

FILE REFERENCE: 98201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT PFILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SEQ ID NO 918

LENGTH: 1453

TYPE: PAT

CORGANISM: rat

US-10-784-004-918
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US-10-784-004-918
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Sequence 950, Application US/10784004

Publication No. US20060084066A1

GENERAL INFORMATION:

APPLICANT: Blogen Idec

TITLE OF INVENTION: Surrogate Markers of Pain

FILE REFERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: Patentin version 3.2

SEQ ID NO 950

RESULT 9 US-10-784-004-950

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                                                                                                                                                                                         1269 QGCNLDAIKVYCNMETGQTCVPPTQPSVPQKNWYISPNPKEKKHVWFGESMTDGFQFEYG 1328
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                                                                                   3 DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPN
                                                                                                                                                                    63 QCCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG
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                                          Gaps
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; Sequence 3, Application US/11202057
; Publication No. US20060051794A1
; GENERAL INFORMATION:
; APPLICANT: TSAL, SHIH-FENG
; APPLICANT: CHEN, WEI-MING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO COL2A1 GENE
; TITLE OF INVENTION: METHODS AND OSTEONECROSIS
; FILE REFERENCE: 08842.0011-00000
; CURRENT APPLICATION NUMBER: US/11/202,057
; CURRENT FILING DATE: 2005-08-12
; PRIOR FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 3
; LEWICH: 1487
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    Length 1453;
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                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.9%; Score 982.5; DB 7; 69.1%; Pred. No. 2.1e-84;
Query Match 93.2%; Score 1238; DB 6; Best Local Similarity 91.0%; Pred. No. 1.4e-108; Matches 223; Conservative 13; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.9%; Score 982.5; Di
Best Local Similarity 69.1%; Pred. No. 2.1e-6
Matches 172; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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Matches 155; Conservative
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1479 VDIGPVCFL 1487
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 ; ORGANISM: Homo sapiens
US-11-202-057-7
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US-11-202-057-28
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Best Local Similarity
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US-11-202-057-28
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                                                                                                         Sequence 5, Application US/11202057

Sequence 5, Application US/11202057

Publication No. US20060051794A1

GENERAL INFORMATION:
APPLICANT: LIU, YU-FEN
APPLICANT: LIU, YU-FEN
TITLE OF INVENTION: MUTATIONS AND COMPOSITIONS RELATING TO COLZA1 GENE
TITLE OF INVENTION: MUTATIONS AND OSTEONECROSIS
TITLE OF INVENTION: MUTATIONS AND US/11/202,057
CURRENT APPLICATION NUMBER: 00/602,319
PRIOR PILLING DATE: 2006-08-12
PRIOR PLILING DATE: 2006-08-18
PRIOR PLILING DATE: 2006-08-18
NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTI VET: 3.2
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Sequence 7, Application No. US20060051794A1

GENERAL INFORMATION:

APPLICANT: TSAI, SHHH-FENG

APPLICANT: LIU, YU-FEN

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO COLZAI GENE

TITLE OF INVENTION: METHODS AND OSTEONECROSIS

TITLE OF INVENTION: MUTATIONS AND OSTEONECROSIS

TITLE OF INVENTION: MUTATIONS AND OSTEONECROSIS

CURRENT APPLICATION NUMBER: US/11/202,057

CURRENT FILING DATE: 2005-008-12

PRIOR PILING DATE: 2005-008-18

NUMBER OF SEQ ID NOS: 114

SOOTWARE: PATCHIN VEY: 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.9%; Score 982.5; DB 7; Length 1487; 69.1%; Pred. No. 2.1e-84; tive 36; Mismatches 38; Indels 3;
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1479 VDIGPVCFL 1487
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239 FDVGPVCFL 247
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Best Local Similarity
Matches 172; Conservat
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1487
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TYPE: PRT
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59 IDPNOGCNIDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQ 118
                                                                                                                                                                                                                                                                                                                   119 FEYGGGGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQQTGNLKKALLLKGSNE 178
                                                                                                                                                                                                                                                                                                                                                                                                                          179 IEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 NITYHCKNSIAYLDEAAGNLKKALLIQGSNDVEIRAEGNSRFTYTALKDGCTKHTGKWGK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 PSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYGGQGSDPADVAIQLTFLRLMSTEASQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 NITYHCKNSVAYMDQQTGNLKKALLLKGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IRSPEGSRKNPARTCRDLKLCHPEWKSGDYWIDPNQGCTLDAMKVFCNMSTGETCVYPNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 IRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMETGETCVYPTQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/11202057

Publication No. US20060051794A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LIU, YU-FEN

APPLICANT: CHEN, WEI-MING

TITLE OF INVENTION: MUTAFIDOS AND COMPOSITIONS RELATING

TITLE OF INVENTION: MUTAFIDOS AND OSTEONECROSIS

CURRENT APPLICATION NUMBER: 60/602,319

PRIOR PLING DATE: 2005-08-18

PRIOR PLING DATE: 2005-08-18

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTIN Ver. 3.2

SEQ ID NO 28

LENGTH: 218

TYPE: PT.
                                                                                                         1 RSD--ANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYW
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     Length 1487;
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                                                      Indels
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Query Match 73.9%; Score 982.5; DB 7; Best Local Similarity 69.1%; Pred. No. 2.1e-84; Matches 172; Conservative 36; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.7%; Score 912.5; DB 7;
70.8%; Pred. No. 8.3e-79;
tive 32; Mismatches 31;
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LENGTH: 1466

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Sequence 33, Application US/11186284;

Sequence 33, Application US/11186284;

Publication No. US20050266493A1

GENERAL INFORMATION:

APPLICANT: Milennium Pharmaceuticals, Inc.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Gamatkar, Shubhangi

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Ramatkar, Shubhangi

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Hurgart, Lawrence J.

APPLICANT: Hurgart, Lawrence J.

TITLE OF INVENTION: MCTHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, MURENTION: MCTHODS FOR IDENTIFICATION, ASSESSMENT, FILE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF SOLON CANCER

TITLE OF INVENTION: WUMBER: US/11/186,284

CURRENT APPLICATION NUMBER: US 60/339,971

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR APPLICATION NUMBER: US 60/331,988

PRIOR FILING DATE: 2002-03-05

PRIOR FILING
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Sequence 964, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Andarmani, Susan

TITLE OP INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt_SeQ_genes Version 1.0

SEQ ID NO 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 -IQLTFLRIMSTEASQNITYHCKNSVAYMDQOTGNLKKALLLKGSNEIEIRAEGNSRFTY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 EVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQGCNLDAIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
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64.8%; Score 861.5; DB 6; Length 1166;
Best Local Similarity 66.5%; Pred. No. 4.3e-73;
Matches 157; Conservative 32; Mismatches 44; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                            13 EVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQGCNLDAIKV
                                                                                                                                                                                                                                                                                                                                          192 SVTVDGCTSHTGAWGKTVIEYKTTKSSRLPIIDVAPLDVGAPDQEFGFDVGPVCFL 247
                                                                                                 3; Gaps
                                                              Query Match 64.8%; Score 861.5; DB 7; Length 1466; Best Local Similarity 66.5%; Pred. No. 5.7e-73; Matches 157; Conservative 32; Mismatches 44; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 26, 2006, 16:20:40 Job time : 10.7384 secs
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-33
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